

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 90.6763 Seconds
(without alignments)
2341.642 Million cell updates/sec

Title: US-09-972-268-4

Perfect score: 2905

Sequence: 1 MARTPGSPICPGGKQALS.....EDDLVSHVDGVSIRREWYV 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2905 | 100.0 | 549 | 5 | Aae23282 Mouse nec |
| 2 | 2887 | 99.4 | 549 | 5 | Aae23283 Human nec |
| 3 | 2887 | 99.4 | 549 | 6 | Abj20222 Human IG |
| 4 | 2887 | 99.4 | 549 | 8 | Adf66369 Human pro |
| 5 | 2887 | 99.4 | 549 | 8 | Adf66711 Human pro |
| 6 | 2866 | 98.7 | 542 | 5 | Aae23281 Human del |
| 7 | 2856 | 98.3 | 555 | 4 | Aam39143 Human pol |
| 8 | 2739 | 94.3 | 549 | 4 | Aag63982 Amino aci |
| 9 | 2739 | 94.3 | 549 | 4 | Aag63985 Amino aci |
| 10 | 2739 | 94.3 | 549 | 5 | Aae23291 Mouse nec |
| 11 | 2568 | 88.4 | 559 | 4 | Aam40929 Human pol |
| 12 | 2138 | 73.6 | 426 | 5 | Aae23289 Human nec |
| 13 | 2138 | 73.6 | 634 | 5 | Aae23287 Human nec |
| 14 | 1924 | 66.2 | 510 | 5 | Aae23285 Mouse nec |
| 15 | 1907 | 65.6 | 595 | 5 | Aae23288 Human nec |
| 16 | 1906 | 65.6 | 510 | 5 | Aae23286 Human nec |
| 17 | 1896 | 65.3 | 387 | 5 | Aae23290 Human nec |
| 18 | 1892 | 65.1 | 504 | 5 | Aae23284 Human del |
| 19 | 1888 | 65.0 | 437 | 5 | Aae23299 Human nec |
| 20 | 1832 | 63.1 | 510 | 4 | Aag63983 Amino aci |
| 21 | 1832 | 63.1 | 510 | 5 | Aae23292 Mouse nec |
| 22 | 1827 | 62.9 | 438 | 4 | Aag63984 Amino aci |
| 23 | 1827 | 62.9 | 438 | 5 | Aae23293 Mouse nec |
| 24 | 1621 | 55.8 | 305 | 5 | Adf41425 Human CD- |
| 25 | 1355 | 46.6 | 258 | 5 | Abb90250 Human pol |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 1235 | 42.5 | 267 | 4 | Aam93536 Human pol |
| 27 | 1235 | 42.5 | 267 | 8 | Adl31248 Human pro |
| 28 | 649.5 | 22.4 | 514 | 6 | Abj20237 Human IG |
| 29 | 649.5 | 22.4 | 517 | 3 | Aay32390 Herpesvir |
| 30 | 649.5 | 22.4 | 517 | 3 | Aae23294 Human nec |
| 31 | 627 | 21.6 | 518 | 5 | Abg77170 Prostate |
| 32 | 569 | 19.6 | 458 | 5 | Aae23295 Human nec |
| 33 | 555.5 | 19.1 | 581 | 8 | Adp03590 Infection |
| 34 | 551 | 19.0 | 580 | 8 | Ado47877 Alpha-Her |
| 35 | 548 | 18.9 | 510 | 8 | Adk83174 Human 191 |
| 36 | 548 | 18.9 | 510 | 8 | Adk83200 Human 191 |
| 37 | 544 | 18.7 | 510 | 4 | Aau00471 Human TAN |
| 38 | 544 | 18.7 | 510 | 5 | Abj05562 Breast ca |
| 39 | 544 | 18.7 | 510 | 6 | Abf48229 Human bla |
| 40 | 544 | 18.7 | 510 | 6 | Abu56613 Lung canc |
| 41 | 544 | 18.7 | 510 | 6 | Abp97212 Tumour-as |
| 42 | 544 | 18.7 | 510 | 7 | Adb80512 Ovarian c |
| 43 | 544 | 18.7 | 510 | 7 | Adm42033 Human TAN |
| 44 | 544 | 18.7 | 510 | 7 | Adn38748 Cancer/an |
| 45 | 544 | 18.7 | 510 | 8 | Adk83210 Human Ig |

ALIGNMENTS

RESULT 1

AAE23282

ID AAE23282 standard; protein; 549 AA.

XX AAE23282;

XX 29-AUG-2003 (revised)

DT 27-AUG-2002 (first entry)

XX

DE Mouse nectin-3-human nectin 3alpha fusion protein.

XX

KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse; stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein; chromosome 3.

XX

OS Homo sapiens.

OS Mus musculus.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Region 1..7

FT Region /note= "Mouse nectin-3 protein"

FT Region 8..549

XX /note= "Human nectin-3alpha protein"

PN WO200228902-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US031392.

XX

PR 05-OCT-2000; 2000US-0238557P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX

DR WPI; 2002-426103/45.

XX

DR N-PSDB; AAD37441.

XX

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria,

PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

PT sepsis, stroke.

XX

| | | |
|----|--|--|
| PS | Claim 1; Page 80-82; 141pp; English. | |
| XX | | |
| CC | The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3 alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to standardise OS field) | |
| XX | | |
| SQ | Sequence 549 AA; | |
| | Query Match 100.0%; Score 2905; DB 5; Length 549; | |
| | Best Local Similarity 100.0%; Pred. No. 1.1e-235; | |
| | Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 MARTPGSPICPGGKAQLSSASLLGALLLPPTPPPLLLLPFLLSRLCAGLAGPI 60 | |
| DB | 1 MARTPGSPICPGGKAQLSSASLLGALLLPPTPPPLLLLPFLLSRLCAGLAGPI 60 | |
| QY | 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAHHPOYGFSGVQYGR 120 | |
| DB | 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAHHPOYGFSGVQYGR 120 | |
| QY | 121 VLFKNYSINDATITLHNIGFSDSGKIYCKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180 | |
| DB | 121 VLFKNYSINDATITLHNIGFSDSGKIYCKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180 | |
| QY | 181 LIDGGNETVAACIAATGKPAHIDWEGDLGEMSTTTSPNETATIIISQYKLPPTRFAR 240 | |
| DB | 181 LIDGGNETVAACIAATGKPAHIDWEGDLGEMSTTTSPNETATIIISQYKLPPTRFAR 240 | |
| QY | 241 GRRITCVVHPALEKDIRYGFILDIQVAPEVSVTGYDGNWFGKGVNLCNADANPPPF 300 | |
| DB | 241 GRRITCVVHPALEKDIRYGFILDIQVAPEVSVTGYDGNWFGKGVNLCNADANPPPF 300 | |
| QY | 301 KSVWSRLDGGWPDLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDOKVIYISDPPT 360 | |
| DB | 301 KSVWSRLDGGWPDLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDOKVIYISDPPT 360 | |
| QY | 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFVLVS 420 | |
| DB | 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFVLVS 420 | |
| QY | 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELSDYSPSVKCNKNPVNN 480 | |
| DB | 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELSDYSPSVKCNKNPVNN 480 | |
| QY | 481 LIRKDYLEEKPTQWNNVNLNRRFERDMYVEDIKMGKFFVSDHYDENEDDLVSHVDGS 540 | |
| DB | 481 LIRKDYLEEKPTQWNNVNLNRRFERDMYVEDIKMGKFFVSDHYDENEDDLVSHVDGS 540 | |
| QY | 541 VISREWV 549 | |
| DB | 541 VISREWV 549 | |
| | RESULT 2 | |
| | AAE23283 | |

| | | |
|----|---|--|
| ID | AAE23283 standard; protein; 549 AA. | |
| XX | | |
| AC | AAE23283; | |
| XX | | |
| DT | 27-AUG-2002 (first entry) | |
| XX | | |
| DE | Human nectin-3alpha protein. | |
| XX | | |
| KW | Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| FT | Key Location/Qualifiers | |
| FT | Modified-site 73 /note= "N-glycosylated" | |
| FT | Domain 74..152 /note= "Extracellular Ig domain" | |
| FT | Modified-site 83 /note= "N-glycosylated" | |
| FT | Modified-site 125 /note= "N-glycosylated" | |
| FT | Modified-site 186 /note= "N-glycosylated" | |
| FT | Domain 189..250 /note= "Extracellular Ig domain" | |
| FT | Modified-site 222 /note= "N-glycosylated" | |
| FT | Domain 287..342 /note= "Extracellular Ig domain" | |
| FT | Modified-site 331 /note= "N-glycosylated" | |
| FT | Domain 405..424 /note= "Transmembrane domain" | |
| FT | Domain 425..549 /note= "C-terminal domain" | |
| XX | | |
| PN | W0200228902-A2. | |
| XX | | |
| PD | 11-APR-2002. | |
| XX | | |
| PF | 05-OCT-2001; 2001WO-US031392. | |
| XX | | |
| PR | 05-OCT-2000; 2000US-0238557P. | |
| XX | | |
| PA | (IMMUNEX) IMMUNEX CORP. | |
| XX | | |
| PI | Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A; | |
| XX | | |
| DR | WPI; 2002-426103/45. | |
| DR | N-PSDB; AAD37442. | |
| XX | | |
| PT | Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke. | |
| PT | | |
| PS | Claim 1; Page 89-91; 141pp; English. | |
| XX | | |
| CC | The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for | |

CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
CC Human nectin-3alpha gene is located on chromosome 3
XX
SQ Sequence 549 AA;

Query Match 99.4%; Score 2887; DB 5; Length 549;
Best Local Similarity 99.6%; Pred. No. 3.5e-234;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTPGSPCLPCGGKQAQLSSASLLGALLLQPTPPPLLLLLLFSRLCGALAGPI 60
Db 1 MARTLRSPCLPCGGKQAQLSSASLLGALLLQPTPPPLLLLLLFSRLCGALAGPI 60

Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVQGEYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVQGEYQGR 120

Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240

Qy 241 GRRITCVVKGHPALEKDIRYSFILDIQVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVKGHPALEKDIRYSFILDIQVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300

Qy 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVVIISDPPT 360
Db 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVVIISDPPT 360

Qy 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420
Db 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420

Qy 421 VLAGIFCVRRTTRGDFYFAKNYIPPSDMQKESQIDVLQDELDSDPSVKKNKPNVN 480
Db 421 VLAGIFCVRRTTRGDFYFAKNYIPPSDMQKESQIDVLQDELDSDPSVKKNKPNVN 480

Qy 481 LIRKDYLEEPKTOWNVENLRPERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEEPKTOWNVENLRPERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540

Qy 541 VISRREWTV 549
Db 541 VISRREWTV 549

RESULT 3
ABJ20222
ID ABJ20222 standard; protein; 549 AA.
XX
AC ABJ20222;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human IG gene related protein SEQ ID No 45.
XX Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.
XX
OS Homo sapiens.
XX
PW WO200299040-A2.
XX

PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017313.
XX
PR 05-JUN-2001; 2001US-0296076P.
XX
PR 10-OCT-2001; 2001US-0328605P.
PR 22-OCT-2001; 2001US-0338733P.
PR 15-FEB-2002; 2002US-0357253P.
PR 15-FEB-2002; 2002US-0357600P.
XX
PA (EXEL-) EXELIXIS INC.
XX
XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Lioubin MN;
XX
DR WPI; 2003-148660/14.
XX
XX Identifying a candidate p53 pathway modulators that are useful as targets
PT for therapeutics or for diagnosing cancers associated with defective p53
PT function, by providing an assay system having a purified IG polypeptide
PT or nucleic acid.
XX
PS Claim 13; Page 206-209; 248pp; English.
XX
XX The invention relates to a novel method for identifying a candidate p53
CC pathway modulating agent. The method comprises providing an assay system
CC having a purified IG polypeptide or nucleic acid, or their functionally
CC active fragment or derivative. The method is useful for identifying
CC modulators of the p53 pathway, particularly for identifying agents for
CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
CC cancer or cancer of the ovary) associated with defective p53 function.
CC The identified modulators are useful as targets for novel therapeutics.
CC The method is also useful for diagnosing disorders associated with
CC defective p53 function. The IG proteins or nucleic acids are useful as
CC modifiers of the p53 pathway, and as therapeutic targets for disorders
CC associated with defective p53 function. This sequence represents a human
CC protein relating to the human IG genes used in the assay for identifying
CC modulators of the p53 pathway of the invention
XX
SQ Sequence 549 AA;

Query Match 99.4%; Score 2887; DB 6; Length 549;
Best Local Similarity 99.6%; Pred. No. 3.5e-234;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTPGSPCLPCGGKQAQLSSASLLGALLLQPTPPPLLLLLLFSRLCGALAGPI 60
Db 1 MARTLRSPCLPCGGKQAQLSSASLLGALLLQPTPPPLLLLLLFSRLCGALAGPI 60

Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVQGEYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVQGEYQGR 120

Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240

Qy 241 GRRITCVVKGHPALEKDIRYSFILDIQVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVKGHPALEKDIRYSFILDIQVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300

Qy 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVVIISDPPT 360
Db 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVVIISDPPT 360

Qy 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420
Db 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420

QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSYKKNKPNVNN 480
Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSYKKNKPNVNN 480
QY 481 LIRKDYLEBPEKTQWNNVNNLRFERPMYDYLKMGKVFSDHVDENEDDLVSHVDGS 540
Db 481 LIRKDYLEBPEKTQWNNVNNLRFERPMYDYLKMGKVFSDHVDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549
RESULT 4
ADRE66369
ID ADR66369 standard; protein; 549 AA.
AC ADR66369;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived protein SEQ ID 223 #2.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX
OS Homo sapiens.
XX
FN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
XX
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kimmendorf H, Roepcke S;
PI Xinzhang L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
XX Claim 2; Page 703; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of a
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected

CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 549 AA;
Query Match 99.4%; Score 2887; DB 8; Length 549;
Best Local Similarity 99.6%; Pred. No. 3.5e-234;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARTPGPSPLCPGGGKAQLSSASLLGAGLLLOQPTPPPLLLLLLFFLLLSRLCGALAGPI 60
Db 1 MARTLPSPPLCPGGGKAQLSSASLLGAGLLLOQPTPPPLLLLLLFFLLLSRLCGALAGPI 60
QY 61 IVEPHVTVAVMGKNVSLKCLIEVNETITQISWEKHGKSQTVAVHHHPQYGFVSQGEYQGR 120
Db 61 IVEPHVTVAVMGKNVSLKCLIEVNETITQISWEKHGKSQTVAVHHHPQYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
QY 181 LIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTPPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTPPNETATIIISQYKLPFTRFAR 240
QY 241 GRRITCVVKHPALEKDIRYFSLDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYFSLDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSWWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPT 360
Db 301 KSWWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPT 360
QY 361 TTTLQPTIIQWHPSTADIEDLATEPKKLPPLSLTLATIKDDTIATIIASVVGGLFVLVS 420
Db 361 TTTLQPTIIQWHPSTADIEDLATEPKKLPPLSLTLATIKDDTIATIIASVVGGLFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSYKKNKPNVNN 480
Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSYKKNKPNVNN 480
QY 481 LIRKDYLEBPEKTQWNNVNNLRFERPMYDYLKMGKVFSDHVDENEDDLVSHVDGS 540
Db 481 LIRKDYLEBPEKTQWNNVNNLRFERPMYDYLKMGKVFSDHVDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549
RESULT 5
ADRE66711
ID ADR66711 standard; protein; 549 AA.
XX
AC ADR66711;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived protein SEQ ID 223 #3.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX

| | |
|----|---|
| OS | Homo sapiens. |
| XX | WO2004076614-A2. |
| PN | 10-SEP-2004. |
| XX | 22-FEB-2004; 2004WO-DE000433. |
| PD | 27-FEB-2003; 2003DE-01009985. |
| XX | 14-MAY-2003; 2003DE-01022134. |
| XX | (HINZ/) HINZMANN B. |
| PA | (DAHL/) DAHL E. |
| PA | (ROSE/) ROSENTHAL A. |
| PA | (HERM/) HERMANN K. |
| PA | (PILA/) PILARSKY C. |
| XX | |
| PI | Schmitt B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T; |
| PI | Schmitt A, Beckmann G, Bruemendorf T, Kinemann H, Roepcke S; |
| PI | Xinzhong L, Staub E; |
| XX | WPI; 2004-653386/63. |
| DR | New nucleic acids, and encoded proteins, from prostatic cancer tissue, |
| PT | useful for diagnosis, treatment and in screening for specific binding |
| PT | agents. |
| XX | Claim 2; Page 1205; 1607pp; German. |
| PS | This invention describes novel cytostatic polynucleotide and polypeptide |
| XX | sequences which can be used in a method for diagnosing prostatic cancer |
| CC | or the risk of developing prostatic cancer. Diagnosis is based on |
| CC | determining over transcription or over expression of the sequences in |
| CC | prostatic tissue. Screening for inhibitors of the sequences or detection |
| CC | substances involves a binding assay, any compounds that bind are |
| CC | selected, optionally after deconvolution of mixtures. Detection of a |
| CC | predetermined minimum level of the reporter indicates the presence of |
| CC | tumour cells. Inhibitors can be chosen from antisense oligonucleotides, |
| CC | short-interfering RNA or ribozymes; an organic molecule of molecular |
| CC | weight below 5000, preferably 300, that binds to the polypeptide; an |
| CC | aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the |
| CC | polypeptide, preferably humanised or human; an anti-idiotypic, non-human |
| CC | (monoclonal) antibody directed against Ab or any of the above derivatised |
| CC | with a reporter group, cell toxin, immunostimulatory molecules and/or |
| CC | radioisotope. The polynucleotides are identified in human prostatic |
| CC | cancer by differential expression analysis, using DNA microarrays, |
| CC | between normal and tumorous tissues, with (over)expression being detected |
| CC | by quantitative PCR. Analysis of prostatic cancer samples showed that |
| CC | CD24 was upregulated in many of them. Sections of tissue, isolated from |
| CC | prostatic cancer patients, or subjects at risk, were incubated |
| CC | sequentially with anti-human CD4 murine monoclonal antibodies; |
| CC | biotinylated second antibody; streptavidin-conjugated horseradish |
| CC | peroxidase and then diaminobenzidine as colour former (brown). The |
| CC | samples were counterstained with hemalum (blue). Malignant cells stained |
| CC | strongly but non-malignant cells only weakly. In 15 of 63 samples of |
| CC | adenocarcinoma, membrane and cytoplasmic staining was very strong, and |
| CC | lymph node metastases were also stained. ADR65805-ADR66954 represent the |
| CC | polynucleotide and polypeptide sequences used in the method of the |
| CC | invention. |
| XX | |
| XX | Sequence 549 AA; |
| XX | Query Match 99.4%; Score 2887; DB 8; Length 549; |
| XX | Best Local Similarity 99.6%; Pred. No. 3 5e-234; |
| XX | Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |
| QY | 1 MARTPGSPCLPCGGKQAQLSSASLLGAGLLLPPTPPPLLLLFP LLFSRLCGALAGPI 60 |
| DB | 1 MARTLRPSLPCGGKQAQLSSASLLGAGLLLPPTPPPLLLLFP LLFSRLCGALAGPI 60 |
| QY | 61 IVEPHYTAWGKNVSLKLIENETITQISWEKINGKSQTVAHVHPQVGSVOQEYOGR 120 |
| DB | 61 IVEPHYTAWGKNVSLKLIENETITQISWEKINGKSQTVAHVHPQVGSVOQEYOGR 120 |

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha protein
CC containing 7 amino acids deleted from the N-terminal end. Human nectin-
CC 3alpha gene is located on chromosome 3
XX
SQ Sequence 542 AA;

Query Match 98.7%; Score 2866; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 2e-232;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 SPLCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLPFLRLCGALAGPIIVEPHVT 67
DB 1 SPLCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLPFLRLCGALAGPIIVEPHVT 60
QY 68 AVGKNVSLKCLIEVNETITQISWEKTHGKSQTVAVHHPOYGFSGVQGVLFKNYS 127
DB 61 AVGKNVSLKCLIEVNETITQISWEKTHGKSQTVAVHHPOYGFSGVQGVLFKNYS 120
QY 128 LNDATITLHNIIGFSDSGKICKAVTFPLGNAQSTTTVLVEPTVSLIKGPDLSLDGNE 187
DB 121 LNDATITLHNIIGFSDSGKICKAVTFPLGNAQSTTTVLVEPTVSLIKGPDLSLDGNE 180
QY 188 TVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCV 247
DB 181 TVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCV 240
QY 248 VKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGKGNLKNADANPPPKSVMSRL 307
DB 241 VKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGKGNLKNADANPPPKSVMSRL 300
QY 308 DGQWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQSDQKVIYISDPPTTTLQPT 367
DB 301 DGQWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQSDQKVIYISDPPTTTLQPT 360
QY 368 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIVLVSVLGIFC 427
DB 361 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIVLVSVLGIFC 420
QY 428 YRRRTTRGDFYAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKPNVNNIRKDYL 487
DB 421 YRRRTTRGDFYAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKPNVNNIRKDYL 480
QY 488 EEPKTOVNNVNLNRRPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISRREW 547
DB 481 EEPKTOVNNVNLNRRPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISRREW 540
QY 548 YV 549
DB 541 YV 542

RESULT 7
AAM39143
ID AAM39143 standard; protein; 555 AA.
XX

AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 19-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
(HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
WPI: 2001-442253/47.
DR N-PSDB; AAI58239.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2288; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 555 AA;
Query Match 98.3%; Score 2856; DB 4; Length 555;
Best Local Similarity 99.8%; Pred. No. 1.4e-231;
Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 PLCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLPFLRLCGALAGPIIVEPHVTA 68
DB 15 PLCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLPFLRLCGALAGPIIVEPHVTA 74
QY 69 VWGKNVSLKCLIEVNETITQISWEKTHGKSQTVAVHHPOYGFSGVQGVLFKNYS 128
XX

Db 75 VMGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQVGFSGVQGEVGRVLPKNSYL 134
 Qy 129 NDATITLHNI GFSDSGKYICKAVTFLPNAQSSITTVLVETVSLIKGPDSLIDGNET 188
 Db 135 NDATITLHNI GFSDSGKYICKAVTFLPNAQSSITTVLVETVSLIKGPDSLIDGNET 194
 Qy 189 VAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRITCV 248
 Db 195 VAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRITCV 254
 Qy 249 KHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPKSVWSRLD 308
 Db 255 KHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPKSVWSRLD 314
 Qy 309 GOWPDGLASONTLHFVHPLTFNYSVYICKVTNSLQORSOKVYIISDPPTTTLQPTI 368
 Db 315 GOWPDGLASONTLHFVHPLTFNYSVYICKVTNSLQORSOKVYIISDPPTTTLQPTI 374
 Qy 369 QWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGGLFVLVSLVLAGIFCY 428
 Db 375 QWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGGLFVLVSLVLAGIFCY 434
 Qy 429 RRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQODELDSYFDSVKKNKPNVNLIRKOYLE 488
 Db 435 RRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQODELDSYFDSVKKNKPNVNLIRKOYLE 494
 Qy 489 EPEKTQWNNVNLNRFPERPMYDIEDLKMGKFPVSDHYDENEDDLVSHVDGVSISRREWY 548
 Db 495 EPEKTQWNNVNLNRFPERPMYDIEDLKMGKFPVSDHYDENEDDLVSHVDGVSISRREWY 554
 Qy 549 V 549
 Db 555 V 555

RESULT 8

AAG63982
 ID AAG63982 standard; protein; 549 AA.

XX AC AAG63982;

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of murine nectin-3.

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

XX Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX 09-MAR-2000; 2000JP-00065595.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX (TAKA/) TAKAHASHI K.

XX Takahashi K, Takai Y, Nakanishi H, Sato K;

XX WPI; 2001-570771/64.

XX N-PSDB; AAH78179.

XX New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and corresponding antibodies.

XX Claim 1; Page 37-40; 64pp; Japanese.

XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic

CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer

XX SQ Sequence 549 AA;

Query Match 94.3%; Score 2739; DB 4; Length 549;

Best Local Similarity 93.3%; Pred. No. 1e-221;

Matches 512; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MARTPGSPCLCPGGKQAQLSASLLGAGLLQLPPTPPLLLLPPLLLFSLCCGALAGPI 60
 Db 1 MARTPGAPLCPGGKQAQLSAPPAAGLLLPAPTPPPLLLLPPLLLFSLCCGALAGSI 60
 Qy 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQVGFSGVQGEVGR 120
 Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQVGFSGVQGEVGR 120
 Qy 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFLPNAQSSITTVLVETVSLIKGPD 180
 Db 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFLPNAQSSITTVLVETVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 Qy 241 GRRITCVVKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFP 300
 Db 241 GRRITCVVKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFP 300
 Qy 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLQORSOKVYIISDPPT 360
 Db 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLQORSOKVYIISDPPT 360
 Qy 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGGLFVLV 420
 Db 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGGLFVLV 420
 Qy 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQODELDSYFDSVKKNKPNV 480
 Db 421 ILAGVFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQODELDSYFDSVKKNKPNV 480
 Qy 481 LIRKDYLEEPEKTKQWNNVNLNRFPERPMYDIEDLKMGKFPVSDHYDENEDDLVSHVD 540
 Db 481 LIRKDYLEEPEKTKQWNNVNLNRFPERPMYDIEDLKMGKFPVSDHYDENEDDLVSHVD 540
 Qy 541 VISRREWYV 549
 Db 541 VISRREWYV 549

RESULT 9

AAG63985

ID AAG63985 standard; protein; 549 AA.

XX AC AAG63985;

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of murine nectin-3.

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

XX Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRPAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRPAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKCNDANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKCNDANPPPF 300
Qy 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIISDPPT 360
Db 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIISDPPT 360
Qy 361 TTTLOPTQIOWHPSADIEDLATEPKLPFPSTLTIKDDTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTQIOWHPSADVEDIATEHKKLGFPPSTLTIKDDTIATIIASVVGALFVLVS 420
Qy 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELSDYPSVKENKNPNVN 480
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELSDYPSVKENKNPNVN 480
Qy 481 LIRKDYLEPEKTOQNNVNNLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVNNLNRPERPMDYYEDLKMGMKFVSDERYNESEDGLVSHVDGS 540
Qy 541 VISRREWTV 549
Db 541 VISRREWTV 549
RESULT 11
AA040929 standard; protein; 559 AA.
XX AA040929;
XX AC AA040929;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 5860.
XX KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX OS Homo sapiens.
XX FN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US034263.
XX PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR N-PSDB; AA160085.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX Example 2; SEQ ID NO 5860; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neotropic, and the
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX Sequence 559 AA;
Qy Query Match 88.4%; Score 2568.5; DB 4; Length 559;
Best Local Similarity 91.3%; Pred. No. 2.6e-207;
Matches 504; Conservative 4; Mismatches 33; Indels 11; Gaps 8;
Qy 9 PLCFGGKAQLSSASLLGAGLLQPPTPPPLLLLLFPLLLSRLCGALAGPIIVEPHVTA 68
Db 8 PLCFGGKAQLSSASLLGAGLLQPPTPPPLLLLLFPLLLSRLCGALAGPIIVEPHVTA 67
Qy 69 VMGRNLSKCLIEVNETITQISWEKIHGKSQTVAVHHPQYGFVQGEYQGRVLFKNYSL 128
Db 68 VMGRNLSKCLIEVNETITQISWEKIHGKSQTVAVHHPQYGFVQGEYQGRVLFKNYSL 127
Qy 129 NDATITLHNTGFSQSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGGNET 188
Db 128 NDATITLHNTGFSQSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGGNET 187
Qy 189 VAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRIITCVV 248
Db 188 VAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRIITCVV 247
Qy 249 KHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKCNDANPPPFKSVWSRLD 308
Db 248 KHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKCNDANPPPFKSVWSRLD 307
Qy 309 GOWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRS-DQKVIISDPPTTTLOP- 366
Db 308 GOWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSPGSKSVTQKVHPTFQDPSLPTYPPL 367
Qy 367 ---TIQW-HPSTADI-EDLATEPKKL-PFPLSTLTIKDDT-IATIIASVVG-GALFIVL 418
Db 368 PALQFQWASPTAXTSRDLATEPKXIAPSPSTLTIKGTQTLPTIIXCSGVGALFIVL 427
Qy 419 VSVLA-GIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELSDYPSVKENKNP 477
Db 428 VKCFGLGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELSDYPSVKENKNP 487
Qy 478 VNNLIRKDYLEPEKTOQNNVNNLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHV 537
Db 488 VNNLIRKDYLEPEKTOQNNVNNLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHV 547
Qy 538 DGSVISRREWTV 549
Db 548 DGSVISRREWTV 559
RESULT 12
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX

[illegible]

CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein containing
 CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
 XX
 SQ Sequence 634 AA;

Query Match 73.6%; Score 2138; DB 5; Length 634;
 Best Local Similarity 100.0%; Pred. No. 6.2e-171; Indels 0; Gaps 0;
 Matches 404; Conservative 0; Mismatches 0;
 Qy 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLPFLFSLCAGLAGPI 60
 Db 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLPFLFSLCAGLAGPI 60
 Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPQYGSVQGEYQGR 120
 Db 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPQYGSVQGEYQGR 120
 Qy 121 VLFKNVSLNDATTILHNIGFSDSGKYICKAVTFFPLGNAQSTTTVLVEPTVSLIKGPD 180
 Db 121 VLFKNVSLNDATTILHNIGFSDSGKYICKAVTFFPLGNAQSTTTVLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
 Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNVFWGKGNLKNADANPPFF 300
 Db 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNVFWGKGNLKNADANPPFF 300
 Qy 301 KSVWSRLDGOWPDGLASDNTLHVFHPLTNYSGVYICKVTNSLGQSDQKVIISDPPT 360
 Db 301 KSVWSRLDGOWPDGLASDNTLHVFHPLTNYSGVYICKVTNSLGQSDQKVIISDPPT 360
 Qy 361 TTTLQPTIQHWPSTADIEDLATEPKLPFLPSTLATIKDDTIAT 404
 Db 361 TTTLQPTIQHWPSTADIEDLATEPKLPFLPSTLATIKDDTIAT 404

RESULT 14
 AAE23285
 ID AAE23285 standard; protein; 510 AA.
 XX
 AC AAE23285;
 XX
 DT 29-AUG-2003 (revised)
 DT 27-AUG-2002 (first entry)
 XX
 DE Mouse nectin-3-human nectin-3beta fusion protein.
 XX
 KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers

FT Region 1..6
 FT /note= "Mouse nectin-3 pprotein"
 FT Region 7..510
 FT /note= "Human nectin-3beta protein"
 XX
 FN WO200228902-A2.
 FN 11-APR-2002.
 XX
 FF 05-OCT-2001; 2001WO-US031392.
 XX
 PR 05-OCT-2000; 2000US-0238557P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 XX
 DR WPI; 2002-426103/45.
 DR N-PSDB; AAD37444.
 XX
 PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX
 PS Claim 1; Page 94-95; 141pp; English.
 XX
 CC The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein encoding 6
 CC amino acids from mouse nectin-3 protein and the rest form human nectin-
 CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 510 AA;

Query Match 66.2%; Score 1924.5; DB 5; Length 510;
 Best Local Similarity 67.9%; Pred. No. 4.5e-153;
 Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
 Qy 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLPFLFSLCAGLAGPI 60
 Db 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLPFLFSLCAGLAGPI 60
 Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPQYGSVQGEYQGR 120
 Db 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPQYGSVQGEYQGR 120
 Qy 121 VLFKNVSLNDATTILHNIGFSDSGKYICKAVTFFPLGNAQSTTTVLVEPTVSLIKGPD 180
 Db 121 VLFKNVSLNDATTILHNIGFSDSGKYICKAVTFFPLGNAQSTTTVLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
 Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNVFWGKGNLKNADANPPFF 300
 Db 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNVFWGKGNLKNADANPPFF 300

Db 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSVTGYDGNWVGRKGVNLKCNADANPPPF 300
QY 301 KSVWSRLDQWPGGLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDPPT 360
Db 301 KSVWSRLDQWPGGLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDVP- 359
QY 361 TTTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDPTIATIASVVGALFVLVLS 420
Db 360 -----FKQTSSAVAGAVIGAVLAFIIA 383
QY 421 VLAGIFCYRRRTFRGDFYAKNY-IPPSDMQKESQIDVLQOQBELDSYDPSVKKENKPV- 478
Db 384 IFVTLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSGPLP 424
QY 479 -NNLIRKDYLEBEKQW-----NNVENLRF-ERPMDYVEDLKMGMKFVSD----- 523
Db 425 QKDLFOPEHL--PLQTFKEREVGNLQHSNGLNSRFDYEDENPNVGEDGIIQQMYPLYNQM 482
QY 524 -----EHVDENEEDLVSHVDGVSISRREWTV 549
Db 483 CYQDRSPGRKHQNNDPKRV-----YIDPREHYV 510

RESULT 15

AAE23288

ID AAE23288 standard; protein; 595 AA.

AC AAE23288;

DT 27-AUG-2002 (first entry)

XX Human nectin-3beta-IgG1Fc region fusion protein.

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.

XX Homo sapiens.

OS Unidentified.

OS Chimeric.

XX WO200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX Claim 9; Page 102-104; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
XX
XX Sequence 595 AA;

Query Match 65.6%; Score 1907; DB 5; Length 595;

Best Local Similarity 76.4%; Pred. No. 1.7e-151;

Matches 383; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLQLQPTPPPLLLLPFLLSRLCGALAGPI 60

Db 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLQLQPTPPPLLLLPFLLSRLCGALAGPI 60

QY 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSQTVAHHHPQYGFVQGEYQGR 120

Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSQTVAHHHPQYGFVQGEYQGR 120

QY 121 VLFKNYSLANDATITLHNGFSDSGKYICKAVTPLGNAOSSTTVTLVEPTVSLIKGPDS 180

Db 121 VLFKNYSLANDATITLHNGFSDSGKYICKAVTPLGNAOSSTTVTLVEPTVSLIKGPDS 180

QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240

Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240

QY 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSVTGYDGNWVGRKGVNLKCNADANPPPF 300

Db 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSVTGYDGNWVGRKGVNLKCNADANPPPF 300

QY 301 KSVWSRLDQWPGGLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDPPT 360

Db 301 KSVWSRLDQWPGGLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDPPT 360

QY 361 TTTTLQ-----PTIQWHPSTADIEDLATEPKLPPLSTLATIKDPTIATII 406

Db 361 KQTSSRSCDKTHTCCPCPAPEAGAPSV-----FLPPPK----PKDTLMISRTPEVTCVV 411

QY 407 ASVVGALFIVLVSLAGIFCYRRRTFRGDYFKNYIPPSDMQKESQIDVLQOQBELDSY 466

Db 412 VDVSHEDEPEVKFNWYDGVGVHNAKTCPREQYNSTY-----RVVSVLTVLHQDWLNGK 465

QY 467 PDSVKKENK---NPVNNLIRK 484

Db 466 EYCKVSNKALPAPIETISK 486

Search completed: October 6, 2005, 09:51:30

Job time : 94.6763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:42:42 ; Search time 18.0493 Seconds
(without alignments)
2926.593 Million cell updates/sec

Title: US-09-972-268-4

Perfect score: 2905

Sequence: 1 MARTPGSPPLCPGGKAQLS.....EDDLVSHVDGVSISRREYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 2141 | 73.7 | 407 | 2 T08732 | hypothetical prote |
| 2 | 627 | 21.6 | 518 | 2 JC4024 | poliovirus recepto |
| 3 | 494 | 17.0 | 467 | 1 HLMS93 | poliovirus recepto |
| 4 | 470 | 16.2 | 530 | 2 A53437 | poliovirus recepto |
| 5 | 463.5 | 16.0 | 478 | 2 I53960 | PRR2 alpha - human |
| 6 | 449.5 | 15.5 | 538 | 2 I68093 | PRR2 delta - human |
| 7 | 422.5 | 14.5 | 417 | 2 A44194 | poliovirus recepto |
| 8 | 415.5 | 14.3 | 392 | 2 B44194 | poliovirus recepto |
| 9 | 390.5 | 13.4 | 392 | 1 RWHUPD | poliovirus recepto |
| 10 | 390.5 | 13.4 | 417 | 1 RWHUPA | poliovirus recepto |
| 11 | 331.5 | 11.4 | 416 | 2 A54017 | colon carcinoma-as |
| 12 | 230.5 | 7.9 | 764 | 2 A49448 | irregular chiasm C |
| 13 | 215.5 | 7.4 | 4391 | 2 A38096 | perlecan precursor |
| 14 | 201 | 6.9 | 5175 | 2 T20992 | hypothetical prote |
| 15 | 201 | 6.9 | 5198 | 2 T43290 | hemichitin precurs |
| 16 | 198 | 6.8 | 588 | 2 JH0506 | adhesion molecule |
| 17 | 194 | 6.7 | 588 | 2 A45294 | surface glycoprote |
| 18 | 189 | 6.5 | 853 | 1 IJUBNC | neural cell adhesi |
| 19 | 187.5 | 6.5 | 274 | 2 A47639 | OX-2 membrane gly |
| 20 | 187.5 | 6.5 | 7962 | 2 I38346 | elastic titin - hu |
| 21 | 182 | 6.3 | 587 | 2 JH0464 | DM-GRASP precurs |
| 22 | 181.5 | 6.2 | 1896 | 2 T08851 | Down syndrome cell |
| 23 | 179 | 6.2 | 3707 | 2 S18252 | heparan sulfate pr |
| 24 | 178.5 | 6.1 | 847 | 2 JH0371 | B-cell adhesion pr |
| 25 | 174 | 6.0 | 858 | 1 IJRTNC | neural cell adhesi |
| 26 | 173.5 | 6.0 | 761 | 1 IJHUNG | neural cell adhesi |
| 27 | 173 | 6.0 | 637 | 2 B33785 | myelin-associated |
| 28 | 172 | 5.9 | 513 | 2 JC5289 | SHP substrate-l pr |
| 29 | 171.5 | 5.9 | 822 | 2 B49151 | fibroblast growth |

| | | | | | |
|----|-------|-----|------|----------|--------------------|
| 30 | 171 | 5.9 | 458 | 2 S23969 | cell-adhesion mole |
| 31 | 171 | 5.9 | 582 | 1 ENRT3S | myelin-associated |
| 32 | 171 | 5.9 | 626 | 1 ENRT3 | myelin-associated |
| 33 | 171 | 5.9 | 1259 | 2 A43425 | Bravo/Nr-CAM cell |
| 34 | 169.5 | 5.8 | 1091 | 1 IJCHNL | neural cell adhesi |
| 35 | 169 | 5.8 | 626 | 1 A61084 | myelin-associated |
| 36 | 168 | 5.8 | 765 | 2 C42632 | cell adhesion mole |
| 37 | 168 | 5.8 | 812 | 2 B42632 | cell adhesion mole |
| 38 | 168 | 5.8 | 932 | 2 A42632 | cell adhesion mole |
| 39 | 166.5 | 5.7 | 822 | 2 S19947 | fibroblast growth |
| 40 | 166 | 5.7 | 739 | 2 JN0581 | vascular cell adhe |
| 41 | 165 | 5.7 | 725 | 1 IJMSNG | neural cell adhesi |
| 42 | 165 | 5.7 | 1115 | 1 IJMSNL | neural cell adhesi |
| 43 | 164.5 | 5.7 | 569 | 2 A46462 | T cell activation |
| 44 | 164 | 5.6 | 521 | 2 JC1508 | biliary glycoprote |
| 45 | 163 | 5.6 | 458 | 1 WMSRI | biliary glycoprote |

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKFP566B0846.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08732

R/Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16474

A:Accession: T08732

A:Molecule type: mRNA

A:Residues: 1-407 <OTT>

A/Cross-references: UNIPROT:Q9Y412; EMBL:AL050071

A/Experimental source: fetal kidney; clone DKFP566B0846

C/Genetics:

A>Note: DKFP566B0846.1

Query Match 73.7%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 5.8e-146;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

| | | | |
|----------|-----|--|-----|
| Qy | 143 | SGKYICKAVTFPLGNAQSSTTVLVEPTVSLIKGPDLSIDGGNETVAAICIAATGK | 202 |
| Db | 1 | SGKYICKAVTFPLGNAQSSTTVLVEPTVSLIKGPDLSIDGGNETVAAICIAATGK | 60 |
| Qy | 203 | HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFI | 262 |
| Db | 61 | HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFI | 120 |
| Qy | 263 | LDIOYAPEVSVTGYDGNWFGVRKGVNLKCNADANPPPPFKSVWSRLDQWPDGLLASNTL | 322 |
| Db | 121 | LDIOYAPEVSVTGYDGNWFGVRKGVNLKCNADANPPPPFKSVWSRLDQWPDGLLASNTL | 180 |
| Qy | 323 | HFVHPLTFNYSYGVYICKVTNSLQORSOKYIYISDPPTTTTLOPTIQWHPSTADIEDLAT | 382 |
| Db | 181 | HFVHPLTFNYSYGVYICKVTNSLQORSOKYIYISDPPTTTTLOPTIQWHPSTADIEDLAT | 240 |
| Qy | 383 | EPKKLPPLSLTATIKDDTIATIIASVVGALFTVLVSVLGIFCYRRRTFRGDYFAXN | 442 |
| Db | 241 | EPKKLPPLSLTATIKDDTIATIIASVVGALFTVLVSVLGIFCYRRRTFRGDYFAXN | 300 |
| Qy | 443 | YIPPSDMQKESQIDVLQDQELSDYPSVSKKNKPNVNNLIRKDYLEPEKTMNNVENLN | 502 |
| Db | 301 | YIPPSDMQKESQIDVLQDQELSDYPSVSKKNKPNVNNLIRKDYLEPEKTMNNVENLN | 360 |
| Qy | 503 | RFRPMDYYEDLKWGMKFVSDHYDENEDDLVSHVDGVSISRREYV | 549 |
| Db | 361 | RFRPMDYYEDLKWGMKFVSDHYDENEDDLVSHVDGVSISRREYV | 407 |
| RESULT 2 | | | |
| JC4024 | | | |


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Db 13 PPTP-----LLWPLLLLLLLETAQAQVRVQVLPVVRQGLGGTVLPCPLLPPVGLYISL 67
Qy 89 ISKEKHGKSS-QTVAVHHPOYGFSGVQGEYQ--RVLF-----KNYSINDATITL 135
Db 68 VTWRDPANHANQVAFHFKMGSPFPSPKPGSERLSFVSAKOSTGQDTAEALQDATLAL 127
Qy 136 HNIQFSDSGKYIKAVTFPLGNAQSSTTVTLVLEP-----TVSLIKGPDLSLDGNET 188
Db 128 HGLTVEDEGNYTCEFATFPKGSVRGWTWLVIAKPKNAQAKVTFSDP-----T 178
Qy 189 VAAICIAATKGPVAHI-----DWEGDLGEMESTTTSPNETATIIISQYKLFPTFRFARG 242
Db 179 TVALCISKEGRPARISWLSLSDWEAKETQVSGTLAG-----TVTVTSRFTLVPSGRADGV 234
Qy 243 RITCVKHPALEKDIRSFILDTQYAPAEVSVTVGDNWVGRKGNLKNADANPPFPKS 302
Db 235 TVTCKVEHESFEFPALIPVTLVRYPEVSVISGVDNWLGRDTATLSCDVRNPPBTGY 294
Qy 303 VWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGVICKVINSLGORSQDKVIYISDPPTTT 362
Db 295 DNSTTSTFTPSAVAQSQL-VIHAVDSLENTFVCTVNAVGMGRABQVIFVRETPNTA 353
Qy 363 TLOPTIQWHPSTADIEDLATEPKLPPPLSLATIKDDTIATIIASVVGALFVLVSVL 422
Db 354 GAGAT-----GGIIGGIIAIIATAV 374
Qy 423 A-GIFCYRRR---TFRGDYPAK-----NYIPPSDMQKESQIDVLQDELSYDPSVK 471
Db 375 AATGILICROORKEQTLQGAEBEDELGGPPSYKPPPTPAK-----LEAQEMPSQLFTLG 428
Qy 472 KENKNPNVNLIRKDYLE-----EPEKTQWNVENLNRPFRPM----- 508
Db 429 ASEHSP-----LKTPYFDAGASCTEQEMPRYHEUPTLEERSGPHLPGATSLGSPVPPGP 484
Qy 509 DYVEDLKMGMKFSDEHYDNEDDL 533
Db 485 PAVEDVSLDLE---DERGEBEEVEYL 506

RESULT 7
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: A44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P32506; GB:S48777
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 14.5%; Score 422.5; DB 2; Length 417;
Best Local Similarity 28.4%; Pred. No. 1.3e-22;
Matches 126; Conservative 68; Mismatches 175; Indels 75; Gaps 17;

Qy 37 PPLLLLLPPLLSRLCGALAGPIIVE--PHVTAVGNKNSLKLIEV---NET-ITQIS 90
Db 10 PPLLLTLEL-----SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT 65
Qy 91 WEKHGKSSQTVAVHH---POYGFSGVQGEYQGRVLFKNYSINDATITLHNIQFSDSGKYI 147
Db 66 WSR-HGESGSMVAFHQYQGNYSPEKRLFVFAARL--GTELRDASLRMFGRLVEDEGNYT 122
Qy 148 CKAVTTPFLGNAQSSTTVTLVLEP--TVSLIKGPDLSLDGNETVAAICIAATKGPVAHID 205
Db 123 CLFVTFPQGSRSVDIWLRLVLAQPNTAEVQVQLT-----GKPVFVARCVSTGGRRPPAHIT 178
Qy 206 WEGDLGEMESTTTSPNETATIIISQYKLFPTFRFARGRITCVVHKHPALEKDIRYSFIL 263
Db 179 WMSDLGGMNPTSQAQGLSGFTVTVSLWILVPSQVDGKSVTCCKVEHESKEPKQLLTNL 238
Qy 264 DIQYAPAEVSVTVGDNWVGRKGNLKNADANPPFPKSVWSRLDQWPDGLLASDNTLH 323
Db 239 TVYYPEVSVISGVDNWNWYLSQNEATLTCDAARSNEPTGYNWSITTMGFLPPFAVAQAGL- 297
Qy 324 FVHPLTFNYSVGVICKVINSLGORSQDKVIYISDPPTTTTLOPTIQWHPSTADIEDLATE 383
Db 298 LIRPVDKPIINTTFCNVTNALGARQAELTVQVKEGP-----PS-----E 336
Qy 384 PKLPPPLSLATIKDDTIATIIASVVGALFVLVSVLAGIFCYRRR---RTF----- 434
Db 337 PSCMSSNI-----IIFLIGIVILLTLGI--GVFYRSRCSREFLWCHHLS 381
Qy 435 -----RGDYFAKNYIPPSDMQKES 453
Db 382 PSSEEHASASANGYISYSDVSRREA 405

RESULT 8
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:P32506; GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 14.3%; Score 415.5; DB 2; Length 392;
Best Local Similarity 28.1%; Pred. No. 3.9e-22;
Matches 121; Conservative 72; Mismatches 174; Indels 63; Gaps 16;

Qy 37 PPLLLLLPPLLSRLCGALAGPIIVE--PHVTAVGNKNSLKLIEV---NET-ITQIS 90
Db 10 PPLLLTLEL-----SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT 65
Qy 91 WEKHGKSSQTVAVHH---POYGFSGVQGEYQGRVLFKNYSINDATITLHNIQFSDSGKYI 147
Db 66 WSR-HGESGSMVAFHQYQGNYSPEKRLFVFAARL--GTELRDASLRMFGRLVEDEGNYT 122
Qy 148 CKAVTTPFLGNAQSSTTVTLVLEP--TVSLIKGPDLSLDGNETVAAICIAATKGPVAHID 205
Db 123 CLFVTFPQGSRSVDIWLRLVLAQPNTAEVQVQLT-----GKPVFVARCVSTGGRRPPAHIT 178
Qy 206 WEGDLGEMESTTTSPNETATIIISQYKLFPTFRFARGRITCVVHKHPALEKDIRYSFIL 263
Db 179 WMSDLGGMNPTSQAQGLSGFTVTVSLWILVPSQVDGKSVTCCKVEHESKEPKQLLTNL 238
Qy 264 DIQYAPAEVSVTVGDNWVGRKGNLKNADANPPFPKSVWSRLDQWPDGLLASDNTLH 323
Db 239 TVYYPEVSVISGVDNWNWYLSQNEATLTCDAARSNEPTGYNWSITTMGFLPPFAVAQAGL- 297
Qy 324 FVHPLTFNYSVGVICKVINSLGORSQDKVIYISDPPTTTTLOPTIQWHPSTADIEDLATE 383
Db 298 LIRPVDKPIINTTFCNVTNALGARQAELTVQVKEGP-----PS-----E 336
Qy 384 PKLPPPLSLATIKDDTIATIIASVVGALFVLVSVLAGIFCYRRRRTFRGDFYFKNY 443
Db 337 PSCMSSNI-----IIFLIGIVILLTLGI--GVFYRSRCS--REFLWCHH 379
Qy 444 IPPSDMQKES 453

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Qy 206 WEGDLGEMESTTTSPNETATIIISQYKLFPTFRFARGRITCVVHKHPALEKDIRYSFIL 263
Db 179 WMSDLGGMNPTSQAQGLSGFTVTVSLWILVPSQVDGKSVTCCKVEHESKEPKQLLTNL 238
Qy 264 DIQYAPAEVSVTVGDNWVGRKGNLKNADANPPFPKSVWSRLDQWPDGLLASDNTLH 323
Db 239 TVYYPEVSVISGVDNWNWYLSQNEATLTCDAARSNEPTGYNWSITTMGFLPPFAVAQAGL- 297
Qy 324 FVHPLTFNYSVGVICKVINSLGORSQDKVIYISDPPTTTTLOPTIQWHPSTADIEDLATE 383
Db 298 LIRPVDKPIINTTFCNVTNALGARQAELTVQVKEGP-----PS-----E 336
Qy 384 PKLPPPLSLATIKDDTIATIIASVVGALFVLVSVLAGIFCYRRR---RTF----- 434
Db 337 PSCMSSNI-----IIFLIGIVILLTLGI--GVFYRSRCSREFLWCHHLS 381
Qy 435 -----RGDYFAKNYIPPSDMQKES 453
Db 382 PSSEEHASASANGYISYSDVSRREA 405

RESULT 8
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:P32506; GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 14.3%; Score 415.5; DB 2; Length 392;
Best Local Similarity 28.1%; Pred. No. 3.9e-22;
Matches 121; Conservative 72; Mismatches 174; Indels 63; Gaps 16;

Qy 37 PPLLLLLPPLLSRLCGALAGPIIVE--PHVTAVGNKNSLKLIEV---NET-ITQIS 90
Db 10 PPLLLTLEL-----SWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLT 65
Qy 91 WEKHGKSSQTVAVHH---POYGFSGVQGEYQGRVLFKNYSINDATITLHNIQFSDSGKYI 147
Db 66 WSR-HGESGSMVAFHQYQGNYSPEKRLFVFAARL--GTELRDASLRMFGRLVEDEGNYT 122
Qy 148 CKAVTTPFLGNAQSSTTVTLVLEP--TVSLIKGPDLSLDGNETVAAICIAATKGPVAHID 205
Db 123 CLFVTFPQGSRSVDIWLRLVLAQPNTAEVQVQLT-----GKPVFVARCVSTGGRRPPAHIT 178
Qy 206 WEGDLGEMESTTTSPNETATIIISQYKLFPTFRFARGRITCVVHKHPALEKDIRYSFIL 263
Db 179 WMSDLGGMNPTSQAQGLSGFTVTVSLWILVPSQVDGKSVTCCKVEHESKEPKQLLTNL 238
Qy 264 DIQYAPAEVSVTVGDNWVGRKGNLKNADANPPFPKSVWSRLDQWPDGLLASDNTLH 323
Db 239 TVYYPEVSVISGVDNWNWYLSQNEATLTCDAARSNEPTGYNWSITTMGFLPPFAVAQAGL- 297
Qy 324 FVHPLTFNYSVGVICKVINSLGORSQDKVIYISDPPTTTTLOPTIQWHPSTADIEDLATE 383
Db 298 LIRPVDKPIINTTFCNVTNALGARQAELTVQVKEGP-----PS-----E 336
Qy 384 PKLPPPLSLATIKDDTIATIIASVVGALFVLVSVLAGIFCYRRRRTFRGDFYFKNY 443
Db 337 PSCMSSNI-----IIFLIGIVILLTLGI--GVFYRSRCS--REFLWCHH 379
Qy 444 IPPSDMQKES 453

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Qy 267 YAEVSVGTGDNWFGKGVNLCNADANPPPFKSVWSRLDQWPDGLLASDNTLHFVH 326
Db 242 YPEVSVISGVDNNWYLQNEATLTCDARSPPTGYNWSITMGPLPPFAVQAQAL-LIR 300
Qy 327 PLTFNYSGVVICKVNSLQORSQKVIYISDPPTTTTLQPTQWHPSTADIEDLATEPKK 386
Db 301 PVDKPINTLICNVNLTALGARQBELTVQVKEGP----- 333
Qy 387 LPPLSLTLATIKDITATIATIASVVGALFTVLVSVLAGIFCY 428
Db 334 -PSEHSMSR-----NAIIFVLGILVFLILLGI--GIYF 366

RESULT 11
A54017
colon carcinoma-associated antigen p84 precursor - rat
N;Alternate names: p84 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: A54017; A61206
R;Chadaneau, C.; LeMoullac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994
A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinoma
A;Reference number: A54017; MUID:94253144; PMID:8195207
A;Accession: A54017
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <CHA>
A;Cross-references: UNIPROT:Q7M048; GB:L12025
R;Chadaneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.
Int. J. Cancer 47, 903-908, 1991
A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcinoma
A;Reference number: A61206; MUID:91184910; PMID:2010233
A;Accession: A61206
A;Molecule type: protein
A;Residues: 34-41, 'X', 43-53 <CH2>
A;Note: the residue at position 9 is suggested to be glycosylated asparagine
C;Comment: This 66k protein is detected by monoclonal antibody B4 on colon carcinoma cell
C;Keywords: glycoprotein; membrane protein

Query Match 11.4%; Score 331.5; DB 2; Length 416;
Best Local Similarity 28.1%; Pred. No. 4.4e-16;
Matches 104; Conservative 56; Mismatches 171; Indels 39; Gaps 12;

Qy 8 SPLCPGGKQAQLSASLLGAGLLLOPTPPPLLLLLFSLCGLAGPIIVEPHVT 67
Db 2 APLA-GASRGRVWSAGL-----LRLLLSCTFLKAGGEIA--VOVLNST 44
Qy 68 AVMGKNVSLKLI--EVNETITQISWEKIKSSQTVAVHHPOYGFVSQGEYQGRVLF-K 124
Db 45 GFLGGSTVLHCSLASKDNVITQLTWKRDPDGSPPFACLPQGGPSIDPERVKFLVAK 104
Qy 125 NY-SLNDATTILHNIGFSDGKYICKAVTTPPLGNAQSTTVTLVLEP--TVSLIKGPDLS 181
Db 105 VYEDLRNASLAISNLNVEDEGIYECQIATPTGSKSANVLMKVPARKNTAEALSPSL 164
Qy 182 IDGNETVAICIAATGKPVNIDW-----EGDLGEMESTTSPFNETATIIISQKLPTR 237
Db 165 MPQD-----VAKCISADGHPGRITWSSNVNGSYSEMKETGSSRAPPLQSATSPMCLLARQ 220
Qy 238 FARRRRITCVVKHPALEKDIRYSFILDIQAPEVSVTYGDNWFGKGVNLCNADANP 297
Db 221 MARIPTPAQWNMK--ASRSRTRSPILSLPYPPPEVVISGYEGNWIIGLTNVLNLTCEARSKP 278
Qy 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSG-VYICKVTNSLGRSQDKVIYIS 356
Db 279 PPTNYSWSTATGPLPNSTHFQENGSHLLISTVDLNNNTIFVCKAINALGSGQGQVTLVK 338
Qy 357 D-----PPTT 361
Db 339 EASEILPPTK 348
```

```
RESULT 12
A49448
irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: irrC-roughest protein
C;Species: Drosophila melanogaster
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49448; S34129
R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandstetter, G.
Genes Dev. 7, 2533-2547, 1993
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal projection
A;Reference number: A49448; MUID:94102535; PMID:7503814
A;Accession: A49448
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-764 <RAM>
A;Cross-references: UNIPROT:Q08180; GB:L11040; NID:G304790; PID:G304791; EMBL:Z21641; NII
C;Genetics:
A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein

Query Match 7.9%; Score 230.5; DB 2; Length 764;
Best Local Similarity 19.4%; Pred. No. 1.8e-08;
Matches 118; Conservative 87; Mismatches 177; Indels 227; Gaps 26;

Qy 40 LLLPFLLLFSLRCGAL-AGP-----IIVEPH-VTAVGKNVSLKCLIEVNETITQI 89
Db 1 MLHTMQLLLLATIVGMVRSPTYSYQNFAMFEPQDTAVVGARVTLPCRV-INKQCT-L 58
Qy 90 SWPKIHGSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSL-----NDATTILHNIGFSDS 143
Db 59 QMTK-----DDFGLGTRDLG---FERYAMVGSDEEGYSLDIYPMVLMDDD 102
Qy 144 GKYICKAVTTPPLGNAQSTT---VTVLVEPTVSLIKGPDLSLIDGGNETVAICIAATGKP 200
Db 103 ARYQCQVSPGPEGQPAIRSTFAGTLVLPPEAPKITQGDVIYATADRKKVIECVSVGCKP 162
Qy 201 VAHIDWEGDLG-----EMESTTTTFFNETA-TIISQVKLPFPTRFARRRITCVVKHHPALE 254
Db 163 AAEITWIDGLGNVLTDNIEYTVLPDQRRFTAKSVLRLTPKKEHHTNFSCQAQNTA-D 221
Qy 255 KDIRYSFI-LDIQYAEVSVT-----GYDGNWFGKRG-----VNL 289
Db 222 RTYRSKIRVEVKYAPKVNVMGSLPGGAGGS--VGGAGGGSVHMSTGSRIVEHSQVRL 279
Qy 290 KCANADANPPPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVVI-CKVTNSLGRS 348
Db 280 ECRADANPSPVRYRWFIN-----EPIIGQKTEWIRNVRKFDHDAIVKEVQNSVGKSE 335
Qy 349 DQKVIYISDPPT-----TTTLQPTIQW--HPS----- 373
Db 336 DSETLDISYAPSRQRPQSMEDVGSVSLTCEVDSNFPQEIWIQHPSDRVVGTSTNLT 395
Qy 374 -----ATTIASVVVG---ALFTVLVSVLAGIFCYRRRRTRFRGDYFKNYVIPP 384
Db 396 FSVSNETAGRYCKANVPVGAETADAVYVLKGPSAIGSQRTQYGLVGDTRARIECPASSV 455
Qy 385 KK-----LPPLSLTLATIKD-----TI----- 402
Db 456 PRARHVSWTNFGQEISESCHDYSILVDVPGGVKSTLIIRDQAHYKYNCTVNVNDYG 515
Qy 403 -----ATTIASVVVG---ALFTVLVSVLAGIFCYRRRRTRFRGDYFKNYVIPP 446
Db 516 NDVAETQLQAKKSVLLMTIVGGISVVAFLVLLTILVVVIKCKERT-----KLPP 566
Qy 447 SDMKESQI 455
Db 567 ADVISEHQI 575

RESULT 13
A38096
perlecan precursor - human
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A:Molecule type: DNA
A:Residues: 1-5175 <W12>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: CESP:F15G9.4a
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1

Query Match 6.9%; Score 201; DB 2; Length 5175;
Best Local Similarity 25.4%; Pred. No. 3.7e-05;
Matches 100; Conservative 50; Mismatches 156; Indels 88; Gaps 23;

QY 59 PIIVE-PHYTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGE 116
Db 793 PTIIESPHTVRVNIERQVTLQCL-AVGIPPEIEWOK---GNVLLATLNNPRYTQLADG- 847
QY 117 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 174
Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQQSQTLLMWTLGLVSPVLGH 891
QY 175 IKGPDSLIDGNETVAACIAATGKPVAHIDWEGDLGEMESITTSPPNETATIIISOYKLF 234
Db 892 VPPEEQILIEQDLTLS--CVVVLGTPKPSIVIKDDKPVEE-----GPTIKIEGGGSL 943
QY 235 PTFARGR---RITCVVHKPALEKDIRYSFIL-----DIQYAPE-----VSVTGYDGNW- 280
Db 944 RLGGNPKDEGKYTCIAVSPAGNSTLHINVQLIKKPEFYKPEGGIVFKPTISGMDEKHV 1003
QY 281 -----FVGRKGVNLKCNADANPPPKSVMSRLDGQWP-----DGLLASDNTLHFVH 326
Db 1004 AVNSTHVDLDGEGFAIPCVSSTGTPPI-ITW-YLDGR-PITNSRDTVTADNTL-IVR 1059
QY 327 PLTFNYSYGVICKVNSLQORSQKVIYISDPPTTTTLOPTIQWHSTADIEDLAT---- 382
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTPMISPGQSSF-----NMVVDLFTIPCD 1114
QY 383 ---EPKKL-----PFPLSLATIKDDTIATI 405
Db 1115 VYGDPKPVITWLLDDKPF---TEGVNEDGSLTI 1145

RESULT 15
T43290
hemicentin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43290; T20993; T24734
R:Vogel, B.E.; Hedgecock, E.M.
A:Submitted to the EMBL Data Library, June 1998
A:Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
A:Reference number: Z22396
A:Accession: T43290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5198 <VUG>
A:Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1
R:Sulston, J.
A:Submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20993
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <W1L>
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone F15G9
R:Kershaw, J.
A:Submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-5198 <W12>
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F15G9.4b
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1

Query Match 6.9%; Score 201; DB 2; Length 5198;
Best Local Similarity 25.4%; Pred. No. 3.7e-05;
Matches 100; Conservative 50; Mismatches 156; Indels 88; Gaps 23;

QY 59 PIIVE-PHYTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGE 116
Db 793 PTIIESPHTVRVNIERQVTLQCL-AVGIPPEIEWOK---GNVLLATLNNPRYTQLADG- 847
QY 117 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 174
Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQQSQTLLMWTLGLVSPVLGH 891
QY 175 IKGPDSLIDGNETVAACIAATGKPVAHIDWEGDLGEMESITTSPPNETATIIISOYKLF 234
Db 892 VPPEEQILIEQDLTLS--CVVVLGTPKPSIVIKDDKPVEE-----GPTIKIEGGGSL 943
QY 235 PTFARGR---RITCVVHKPALEKDIRYSFIL-----DIQYAPE-----VSVTGYDGNW- 280
Db 944 RLGGNPKDEGKYTCIAVSPAGNSTLHINVQLIKKPEFYKPEGGIVFKPTISGMDEKHV 1003
QY 281 -----FVGRKGVNLKCNADANPPPKSVMSRLDGQWP-----DGLLASDNTLHFVH 326
Db 1004 AVNSTHVDLDGEGFAIPCVSSTGTPPI-ITW-YLDGR-PITNSRDTVTADNTL-IVR 1059
QY 327 PLTFNYSYGVICKVNSLQORSQKVIYISDPPTTTTLOPTIQWHSTADIEDLAT---- 382
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTPMISPGQSSF-----NMVVDLFTIPCD 1114
QY 383 ---EPKKL-----PFPLSLATIKDDTIATI 405
Db 1115 VYGDPKPVITWLLDDKPF---TEGVNEDGSLTI 1145

Search completed: October 6, 2005, 10:21:06
Job time : 21.0493 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:34:02 ; Search time 81.4368 Seconds
(without alignment)
3452.143 Million cell updates/sec

Title: US-09-972-268-4
Perfect score: 2905
Sequence: 1 MARTPGSPPLCPGGGKAQLS.....EDDLVSHVDSVTSRREMYV 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 2887 | 99.4 | 549 | 2 Q9NQ33 | Q9ng83 homo sapien |
| 2 | 2739 | 94.3 | 549 | 2 Q9JL89 | Q9jlb9 mus musculus |
| 3 | 2695 | 92.8 | 549 | 2 Q9D006 | Q9d006 mus musculus |
| 4 | 2141 | 73.7 | 407 | 2 Q9Y412 | Q9y412 homo sapien |
| 5 | 1858 | 64.0 | 366 | 2 Q6NV23 | Q6nv23 homo sapien |
| 6 | 1832.5 | 63.1 | 510 | 2 Q9JL88 | Q9jlb8 mus musculus |
| 7 | 1827.5 | 62.9 | 438 | 2 Q9JL87 | Q9jlb7 mus musculus |
| 8 | 1629 | 56.1 | 304 | 2 Q9BVA9 | Q9bva9 homo sapien |
| 9 | 1235 | 42.5 | 267 | 2 Q9NC05 | Q9nc05 homo sapien |
| 10 | 659.5 | 22.7 | 515 | 1 PVR1 MOUSE | Q9jlf6 mus musculus |
| 11 | 653.5 | 22.5 | 515 | 2 Q6P9M9 | Q6p9m9 mus musculus |
| 12 | 649.5 | 22.4 | 517 | 1 PVR1 HUMAN | O15223 homo sapien |
| 13 | 641.5 | 22.1 | 515 | 1 PVR1_PIG | Q9gl76 sus scrofa |
| 14 | 544 | 18.7 | 510 | 2 Q96N78 | Q9eny8 homo sapien |
| 15 | 543 | 18.7 | 510 | 2 Q96KJ5 | Q96kl5 homo sapien |
| 16 | 542 | 18.7 | 510 | 2 Q8WVU4 | Q8wvu4 homo sapien |
| 17 | 534.5 | 18.4 | 295 | 2 Q9ER75 | Q9erf5 mesocricetu |
| 18 | 528 | 18.2 | 298 | 2 Q9GL74 | Q9gl74 cercopithec |
| 19 | 526.5 | 18.1 | 295 | 2 Q9GL75 | Q9gl75 bos taurus |
| 20 | 506 | 17.4 | 508 | 2 Q8CEB8 | Q8ced8 mus musculus |
| 21 | 506 | 17.4 | 508 | 2 Q9R007 | Q9r007 mus musculus |
| 22 | 504 | 17.3 | 463 | 2 Q66J72 | Q66j72 xenopus lae |
| 23 | 502.5 | 17.3 | 464 | 2 Q6GL25 | Q6gl25 xenopus tro |
| 24 | 496 | 17.1 | 467 | 2 Q8C6F2 | Q8c6f2 mus musculus |
| 25 | 494 | 17.0 | 467 | 2 Q9IVT9 | Q9ivt9 mus musculus |
| 26 | 493.5 | 17.0 | 483 | 2 Q9DBP8 | Q9dbp8 mus musculus |
| 27 | 474 | 16.3 | 530 | 2 Q80XJ5 | Q80xj5 mus musculus |
| 28 | 470 | 16.2 | 530 | 1 PVR2 MOUSE | P32507 mus musculus |
| 29 | 449.5 | 15.5 | 538 | 1 PVR2 HUMAN | Q92692 homo sapien |
| 30 | 432 | 14.9 | 449 | 2 Q9UE16 | Q9ue16 homo sapien |
| 31 | 423.5 | 14.6 | 400 | 2 Q8HY16 | Q8hy16 cebus apeil |

| | | | | | |
|----|-------|------|-----|-------------|---------------------|
| 32 | 422.5 | 14.5 | 417 | 1 PVR_CERAE | P32506 cercopithec |
| 33 | 413.5 | 14.2 | 412 | 2 Q9RIE1 | Q9riel rattus norv |
| 34 | 408.5 | 14.1 | 412 | 2 Q63611 | Q63611 rattus norv |
| 35 | 400.5 | 13.8 | 401 | 2 Q08835 | Q08835 cercopithec |
| 36 | 393 | 13.5 | 408 | 2 Q91WP1 | Q91wp1 mus musculus |
| 37 | 391.5 | 13.5 | 412 | 2 Q8HY14 | Q8hy14 oryctolagus |
| 38 | 391 | 13.5 | 408 | 2 Q8K094 | Q8k094 m hypotheri |
| 39 | 390.5 | 13.4 | 417 | 1 PVR_HUMAN | P15151 homo sapien |
| 40 | 390 | 13.4 | 408 | 2 Q8BVF6 | Q8bvf6 mus musculus |
| 41 | 381.5 | 13.1 | 403 | 2 Q8HY15 | Q8hy15 lemur catta |
| 42 | 346 | 11.9 | 415 | 2 Q60977 | Q60977 mus musculus |
| 43 | 342.5 | 11.8 | 476 | 2 Q6AYP5 | Q6ayp5 rattus norv |
| 44 | 336.5 | 11.6 | 456 | 2 Q8R5M8 | Q8r5m8 mus musculus |
| 45 | 334.5 | 11.5 | 442 | 2 Q9BY67 | Q9by67 homo sapien |

ALIGNMENTS

RESULT 1

| | | | |
|--------|--|------|---------|
| Q9NQ33 | PRELIMINARY; | PRT; | 549 AA. |
| ID | Q9NQ33 | | |
| AC | Q9NQ33; | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | |
| DE | Nectin 3. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Reymond N., Borg J.-P., Lecocq E., Campadelli-Fiume G., | | |
| RA | Dubreuil P., Lopez M.; | | |
| RT | "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that | | |
| RT | interacts with afadin."; | | |
| RL | Gene 0:0-0(2000). | | |
| DR | EMBL; AF282874; AAF97597.1; -. | | |
| DR | InterPro; IPR003599; Ig. | | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | Pfam; PF00047; Ig; 1. | | |
| DR | SMART; SM00409; Ig; 1. | | |
| DR | PROSITE; PS50835; IG-LIKE; 3. | | |
| DR | SEQUENCE 549 AA; 61002 MW; | | |
| DR | 5D1104CCB4A9D731 CRC64; | | |

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QY 361 TTTTLOPTIOWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
DB 361 TTTTLOPTIOWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKPNVNN 480
DB 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKPNVNN 480
QY 481 LIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLKMGKMFVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLKMGKMFVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
DB 541 VISRREWYV 549

RESULT 2
Q9JLB9 PRELIMINARY; PRT; 549 AA.
ID Q9JLB9
AC Q9JLB9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN Names=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Grachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 60582 MW; 5492C9ABB472F185 CRC64;

Query Match 94.3%; Score 2739; DB 2; Length 549;
Best Local Similarity 93.3%; Pred. No. 6e-196;
Matches 512; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPI 60
DB 1 MARTPGAPLCPGGKQAQLSSAPPAAGLLLPAPTPPPPLLLLPPLLLFSLRCLGALAGSI 60
QY 61 IVEPHVTAVMGKNVSLKLEVNETITQISWEKIHGSSQTVAVHHPOYGFSGVQYQGR 120
DB 61 IVEPHVTAVMGKNVSLKLEVNETITQISWEKIHGSKSTQTVAVHHPOYGFSGVQYQGR 120
QY 121 VLFKNVSLNDATITLHNIGFSDSKYICKAVTPPLGNAQGSTTTVLVEPTVSLIKGPDS 180
DB 121 VLFKNVSLNDATITLHNIGFSDSKYICKAVTPPLGNAQGSTTTVLVEPTVSLIKGPDS 180
QY 181 LIDGGNETVAICAATGKPVAVHDWEGDLGEMESTTSPNETATIIISQYKLPFPTFRAR 240
DB 181 LIDGGNETVAACVAAATGKPVAVHDWEGDLGEMESTTSPNETATIIISQYKLPFPTFRAR 240

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QY 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNFVGRKGVNLKCNADANPPPF 300
DB 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNFVGRKGVNLKCNADANPPPF 300
QY 301 KSVMSLDGQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQORSQOKVIYISDPPT 360
DB 301 KSVMSLDGQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQORSQOKVIYISDPPT 360
QY 361 TTTTLOPTIOWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
DB 361 TTTTLOPTIOWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKPNVNN 480
DB 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKPNVNN 480
QY 481 LIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLKMGKMFVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLKMGKMFVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
DB 541 VISRREWYV 549

RESULT 3
Q9D006 PRELIMINARY; PRT; 549 AA.
ID Q9D006
AC Q9D006;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610301B19 product:poliovirus receptor-related
DE 3, full insert sequence.
GN Names=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Whole body;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matakishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; F:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;
Query Match 92.8%; Score 2695; DB 2; Length 549;
Best Local Similarity 91.8%; Pred. No. 1.2e-192;
Matches 504; Conservative 22; Mismatches 23; Indels 0; Gaps 0;
QY 1 MAREPGSLPCGGKGAQLSSALGALLQPTPPPLLLLPPLLLFRLCGALAGPI 60
DB 1 MAREPGAPLPCGGKGAQLSSAPPAAGLLLPAPTTPPLLLLPPLLLFRLCGALAGSI 60
QY 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKHGKSSQTVAVHPHQYGSVQGEYQGR 120
DB 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKHGKSTQTVAVHPHQYGSVQGEYQGR 120
QY 121 VLFKNYSINDATITLHNIGSDSKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
DB 121 VLFKNYSINDATITLHNIGSDSKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
QY 181 LIQGGNETVAICIAATGKPAHLDWEGDLGEMESTTSPNETATIIISQYKLPPTPFAR 240
DB 181 SIDGGNETVAICVSSGKPAQIDWEGDLGEREFSTISFLNETATIVSQYELPPTPFAR 240
QY 241 GRRITCVVKGPALEKDIRYSFILDIOVAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
DB 241 GRRITCVVKGPALEKDIRYSFILDIOVAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDGGWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYISDPT 360
DB 301 KSVMSRLDGGWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYISDPT 360
QY 361 TTTLQPTQVHSSPADVDQDIATEHKKLPPLSTLATLKDDTIGTIIASVVGALFLVLVS 420

DB 361 TTTLQPTQVHSSPADVDQDIATEHKKLPPLSTLATLKDDTIGTIIASVVGALFLVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPSDMKQESQIDVLQDELDSDYSPDSVKKNKPNVN 480
DB 421 ILAGVFCYRRRTFRGDYFAKNYIPSDMKQESQIDVLQDELDSDYSPDSVKKNKPNVN 480
QY 481 LIRKDYLEPEKQWNNVENLRFERPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEPEKQWNNVENLRFERPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
DB 541 VISRREWYV 549
RESULT 4
QY412 PRELIMINARY; PRT; 407 AA.
AC QY412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp566B0846 (Fragment).
GN Name:DKFZp566B0846;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;
Query Match 73.7%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 1.9e-151;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 143 SGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLDGNETVAAICIAATGKPA 202
DB 1 SGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLDGNETVAAICIAATGKPA 60
QY 203 HIWEGDLGEMESTTSPNETATIIISQYKLPPTPFARGRITCVVKGPALEKDIRYSFI 262
DB 61 HIWEGDLGEMESTTSPNETATIIISQYKLPPTPFARGRITCVVKGPALEKDIRYSFI 120
QY 263 LDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPFKSVMSRLDGGWPDGLASDNTL 322
DB 121 LDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPFKSVMSRLDGGWPDGLASDNTL 180
QY 323 HFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYISDPTTTLQPTIIQWHPSTADIEDLAT 382
DB 181 HFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYISDPTTTLQPTIIQWHPSTADIEDLAT 240
QY 383 EPKKLFPPLSTLATIKDDTIIATIIASVVGALFVLVSLAGIFCYRRRTFRGDYFAKN 442
DB 241 EPKKLFPPLSTLATIKDDTIIATIIASVVGALFVLVSLAGIFCYRRRTFRGDYFAKN 300
QY 443 YIPSDMKQESQIDVLQDELDSDYSPDSVKKNKPNVNLRKDYLEPEKQWNNVENL 502
DB 301 YIPSDMKQESQIDVLQDELDSDYSPDSVKKNKPNVNLRKDYLEPEKQWNNVENL 360
QY 503 RFRPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGSVTSRREWYV 549
DB 361 RFRPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGSVTSRREWYV 407

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| RESULT 5 | |
| Q6NVZ3 | PRELIMINARY; PRT; 366 AA. |
| ID | Q6NVZ3 |
| AC | Q6NVZ3; |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Created) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) |
| DE | PVRL3 protein. |
| GN | Name=PVRL3; |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| OX | NCBI_TaxID=9606; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Brain; |
| RX | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., |
| RA | Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., |
| RA | Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C., |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., |
| RA | Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., |
| RA | Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., |
| RA | Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., |
| RA | Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., |
| RA | Jones S.J., Marra M.A.; |
| RT | "Generation and initial analysis of more than 15,000 full-length human |
| RT | and mouse cDNA sequences."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Brain; |
| RA | Strausberg R.; |
| RL | Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL; BC067808; AAG67808.1; -. |
| DR | InterPro; IPR003599; IG. |
| DR | InterPro; IPR007110; IG-like. |
| DR | Pfam; PF00047; IG; 1. |
| DR | SMART; SM00409; IG; 1. |
| DR | PROSITE; PS50835; IG LIKE; 3. |
| SQ | SEQUENCE 366 AA; 39722 MW; 591D0A4687C630BA CRC64; |
| Query Match 64.0%; Score 1858; DB 2; Length 366; | |
| Best Local Similarity 99.2%; Pred. No. 2.3e-130; | |
| Matches 353; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | |
| Qy | 1 MARTPGSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRCLGALGPI 60 |
| Db | 1 MARTLRESPLCPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRCLGALGPI 60 |
| Qy | 61 IVEPHVTAVWGKNSVLSKCLIEVNETTIQISWEKHGKSSQTVAVHPQYGSVQGEYQGR 120 |
| Db | 61 IVEPHVTAVWGKNSVLSKCLIEVNETTIQISWEKHGKSSQTVAVHPQYGSVQGEYQGR 120 |
| Qy | 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180 |
| Db | 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180 |
| Qy | 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240 |
| Db | 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240 |
| Qy | 241 GRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300 |
| Db | 241 GRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300 |
| Qy | 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVYIISD 360 |
| Db | 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVYIISD 360 |
| Qy | 361 TTTTLOPTIQWHPSTADIEDLATEPKPLPPLPLSTLTIATIKDPTIATIASVVGALFIVLS 420 |
| Db | 361 TTTTLOPTIQWHPSTADIEDLATEPKPLPPLPLSTLTIATIKDPTIATIASVVGALFIVLS 420 |
| Query Match 63.1%; Score 1832.5; DB 2; Length 510; | |
| Best Local Similarity 66.8%; Pred. No. 3e-128; | |
| Matches 376; Conservative 39; Mismatches 81; Indels 67; Gaps 10; | |
| Qy | 1 MARTPGSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRCLGALGPI 60 |
| Db | 1 MARTPGAPLCPGGKQAQLSSAPPPAAGLLLPAPTTPPLLLLPPLLLFSLRCLGALGSI 60 |
| Qy | 61 IVEPHVTAVWGKNSVLSKCLIEVNETTIQISWEKHGKSSQTVAVHPQYGSVQGEYQGR 120 |
| Db | 61 IVEPHVTAVWGKNSVLSKCLIEVNETTIQISWEKHGKSTQTVAVHPQYGSVQGDYQGR 120 |
| Qy | 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180 |
| Db | 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180 |
| Qy | 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240 |
| Db | 181 LIDGGNETVAACVAAATGKPVAAQIDWEGDLGEMESTTSPNETATIVSQYKLPPTFRAR 240 |
| Qy | 241 GRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300 |
| Db | 241 GRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300 |
| Qy | 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVYIISD 360 |
| Db | 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVYIISD 360 |
| Qy | 361 TTTTLOPTIQWHPSTADIEDLATEPKPLPPLPLSTLTIATIKDPTIATIASVVGALFIVLS 420 |
| Db | 361 TTTTLOPTIQWHPSTADIEDLATEPKPLPPLPLSTLTIATIKDPTIATIASVVGALFIVLS 420 |

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Db 361 TQT-----SSIA-----VAGAVIGAVLALFIIT 383
Qy 421 VLAGIFCYRRRTFRGDFYAKNY-IPPSDMQK---ESQIDVLOQDEL-----DSYPDSVKK 472
Db 384 VFTVLLTPRK--RPSYLDKVIDLPPTHKPPVYEEIRPSLPQKDLGQTEHLPLQTQF 441
Qy 473 ENK-----NPVNNLIRKYLEEPEKT-QWNNVNNLNRFRPMDYEDDLKMGKMFVSDEHY 526
Db 442 KEGAGGLQPSNGSPISRRFYEDSTQWEDGTQRMCLPSYQCHODRSR-----OH 494
Qy 527 DENEDDLVSHVDSGVSIRREWYV 549
Db 495 PRNPERL-----YINPREHYV 510

RESULT 7
Q9JLB7
ID Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3, a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; ig; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

Query Match 62.9%; Score 1827.5; DB 2; Length 438;
Best Local Similarity 76.7%; Pred. No. 5.7e-128;
Matches 358; Conservative 25; Mismatches 41; Indels 43; Gaps 5;

Qy 1 MARTPGSPCLPGGKQAQLSSALILGALLQPPPTPLLLLPFLLLFSLRCLGALAGPI 60
Db 1 MARTPGAPLCPGGKQAQLSAPFPAAGLLLPATPPPLLLLPFLLLFSLRCLGALAGSI 60
Qy 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKHGKSQTQVAVHHPQYGSFGVQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKHGKSQTQVAVHHPQYGSFGVQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGYICKATVFPGLNAQSSTTVTLVPTVSLIKGDS 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGYICKATVFPGLNAQSSTTVTLVPTVSLIKGDS 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDILGEMESTTTSFPNETATITISQYKLPFTRPAR 240
Db 181 LIDGNETVAACVAAATGKPAQIDWEGDILGEMESTTTSFPNETATITISQYKLPFTRPAR 240
Qy 241 GRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
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Db 241 GRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPT 360
Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDIPL 360
Qy 361 TTTLOPTIQWHPSTADIEDLATEPKPLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
Db 361 TQT-----SSIA-----VAGAVIGAVLALFIIT 383
Qy 421 VLAGIFCYRRRTFRGDFYAKNY-IPPSDMQK---ESQIDVLOQDEL 463
Db 384 VFTVLLTPRK--RPSYLDKVIDLPPTHKPPVYEEIRPSLPQKDL 428

RESULT 8
Q9BVA9
ID Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nectin 3; DKFZP566B0846 protein (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA TISSUE=Cervix;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER;
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 56.1%; Score 1629; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.3e-113;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVWS 305
Db 1 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVWS 60
Qy 306 RLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPTTTTLQ 365
Db 61 RLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPTTTTLQ 120
Qy 366 PTIQWHPSTADIEDLATEPKPLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS LAGI 425
Db 121 PTIQWHPSTADIEDLATEPKPLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS LAGI 180
Qy 426 FCYRRRTFRGDFYAKNYIPPSDMQKESQIDVLOQDELSDYPSVKKENKPNVNNLIRKD 485
Db 181 FCYRRRTFRGDFYAKNYIPPSDMQKESQIDVLOQDELSDYPSVKKENKPNVNNLIRKD 240
Qy 486 YLEPEKPTQWNNVNNLNRFRPMDYEDDLKMGKMFVSDEHYDENEDDLVSHVDSGVSIRRR 545
Db 241 YLEPEKPTQWNNVNNLNRFRPMDYEDDLKMGKMFVSDEHYDENEDDLVSHVDSGVSIRRR 300
Qy 546 EWYV 549
Db 301 EWYV 304

RESULT 9
Q8NC05
ID Q8NC05 PRELIMINARY; PRT; 267 AA.
AC Q8NC05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

```
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwavanagi T., Ninomiya K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK075105; BAC11404.1; -.
DR GO; GO:0004872; F:receptor activity; ISA.
DR InterPro; IPR007110; Ig-Like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 42.5%; Score 1235; DB 2; Length 267;
Best Local Similarity 96.0%; Pred. No. 5.4e-84;
Matches 242; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 41 LLLFPLL-LFSRLCGALAGPIIPEHVTAVGKNVSLKCLIEVNETITQISWEKINGKS 98
DB 16 LLRGPLLPRFSFGNPRALAGPIIPEHVTAVGKNVSLKCLIEVNETITQISWEKINGKS 75

QY 99 SQTVAHHPOYGSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNA 158
DB 76 SQTVAHHPOYGSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNA 135

QY 159 QSSTVTVLVEPTVSLIKGPDSLIDGNETVAAICATGKPAHIDWEGDLGEMESTTT 218
DB 136 QSSTVTVLVEPTVSLIKGPDSLIDGNETVAAICATGKPAHIDWEGDLGEMESTTT 195

QY 219 SFPNETATISQYKLPFPTRFARGRRITCVVKHPALEKDIRYSFLDITQYAPEVSVTYGDG 278
DB 196 SFPNETATISQYKLPFPTRFARGRRITCVVKHPALEKDIRYSFLDITQYAPEVSVTYGDG 255

QY 279 NWFVGRKGVNLK 290
DB 256 NWFVGRKGVNLK 267

RESULT 10
PVRL_MOUSE STANDARD; PRT; 515 AA.
AC Q9JFK6; Q9ERL5; Q9J117;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1).
GN Names=Pvrl1; Synonyms=HvEC, Prr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RM MEDLINE=2043787; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi P., Adelaide J.,
RA Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin delta serves as a species
RT nonspecific mediator for entry of human and animal alpha herpesviruses
RT in a pathway independent of detectable binding to gD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872 (2000).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RX DOI=10.1128/JVI.74.24.11773-11781.2000;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-1alpha to human nectin-1alpha
RT (HvEC) in sequence and activity as a glycoprotein D receptor for
RT alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the
RT floor plate during embryogenesis, suggesting a role in neural
RT development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Probably involved in cell adhesion. Receptor for
CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
CC cells.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC
CC EMBL; AF239762; AAF60333.1; -.
CC EMBL; AF270977; AAF76195.1; -.
CC EMBL; AF297665; AAG22808.1; -.
CC HSSP; Q05793; 1GL4.
CC GO; GO:0005913; C:cell-cell adherens junction; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0004872; F:receptor activity; IDA.
CC InterPro; IPR007110; Ig-Like.
CC Pfam; PF00047; ig; 2.
CC PROSITE; PS00835; IG_LIKE; 2.
CC Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
CC Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 515 Poliovirus receptor related protein 1.
FT DOMAIN 31 354 Extracellular (Potential).
FT TRANSMEM 355 375 Potential.
FT DOMAIN 376 515 Cytoplasmic (Potential).
FT DOMAIN 31 141 Ig-like V-type.
FT DOMAIN 145 243 Ig-like C2-type 1.
FT DOMAIN 247 334 Ig-like C2-type 2.
FT DOMAIN 436 442 Poly-Glu.
FT DOMAIN 443 447 Poly-Gly.
FT DISULFID 51 124 By similarity.
FT DISULFID 172 226 By similarity.
FT DISULFID 269 316 By similarity.
FT CARBOHYD 36 36 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 72 72 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 139 139 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 202 202 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 286 286 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 297 297 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 332 332 N-linked (GLCNAC...) (Potential).
FT CONFLICT 138 138 L -> P (in Ref. 1).
FT CONFLICT 165 165 N -> D (in Ref. 1).
FT CONFLICT 342 342 P -> PP (in Ref. 2).
FT CONFLICT 428 428 S -> G (in Ref. 3).
SQ SEQUENCE 515 AA; 57064 MW; FFF608E5FFB7A0F CRC64;

Query Match 22.7%; Score 659.5; DB 1; Length 515;
Best Local Similarity 32.5%; Pred. No. 1.4e-40;
```

| | | | | | |
|--|---|---|--|------------|-------------|
| "Generation and initial analysis of more than 15,000 full-length human | | | | | |
| RT | and mouse cDNA sequences." | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002). | | | | |
| RN | {2} | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-C57BL/6; TISSUE=Brain; | | | | |
| RA | Strauberg R.; | | | | |
| RL | Submitted (Nov-2003) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; BC060694; AAH60694.1; - | | | | |
| DR | GO; GO:0005913; C:cell-cell adherens junction; IDA. | | | | |
| DR | GO; GO:0005615; C:extracellular space; TAS. | | | | |
| DR | GO; GO:0016021; C:integral to membrane; TAS. | | | | |
| DR | GO; GO:0005151; F:protein binding; IPI. | | | | |
| DR | GO; GO:0004872; F:receptor activity; IDA. | | | | |
| DR | InterPro; IPR003599; Ig. | | | | |
| DR | InterPro; IPR007110; Ig-like. | | | | |
| DR | InterPro; IPR003598; Ig_c2. | | | | |
| DR | InterPro; IPR003596; Ig_v. | | | | |
| DR | Pfam; PF00047; Ig; 1. | | | | |
| DR | SMART; SM00409; IG; 2. | | | | |
| DR | SMART; SM00408; IGC2; 2. | | | | |
| DR | SMART; SM00406; IGV; 1. | | | | |
| DR | PROSITE; PS50835; IG_LIKE; 2. | | | | |
| KW | Receptor. | | | | |
| SQ | SEQUENCE. 515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64; | | | | |
| | | | | | |
| | Query Match | 22.5%; | Score 653.5; | DB 2; | Length 515; |
| | Best Local Similarity | 32.3%; | Pred. No. 3.9e-40; | | |
| | Matches 169; | Conservative 83; | Mismatches 176; | Indels 95; | Gaps 18; |
| | | | | | |
| Qy | 71 | GKVVSLKCLIE--- | VNETITQISWEKIHGKSQTVAVHHPOYGFVSOGVEYQGRVLFNKYS | 127 | |
| Dd | 44 | GTDVDLHCSPANLPVSKITQVTWQKASGSKQNMAIYNPTMGVSVLPFYEKRVFLRPS | 103 | | |
| | | | | | |
| Qy | 128 | LNDATITLHNIGSDSKYICKAVTPEPLGNAQSSTTVTLVETPVSLIKGPSDSLIDG--- | 184 | | |
| Dd | 104 | FIDGITRLSGLEDEBGMYICEFATPPPTGNRESQLNLTVNAKPT--NWIEGTRAVLRARKG | 162 | | |
| | | | | | |
| Qy | 185 | -GNETVAAICIAATGPVAHIDMEGLD--GMESMTTTSFPNETATIISOYKLFPTRFARGR | 242 | | |
| Dd | 163 | QDDKVLVATCTSANGRPPSAVSNETRLKGAEYQEIRNPNGTWTVISRYRLVPSREAHQ | 222 | | |
| | | | | | |
| Qy | 243 | RITCVVKHPALEKDRIYSFDILOQAPEVSVTGVDGNWFVGRKGVNLIKCNADANPPPFSK | 302 | | |
| Dd | 223 | SLACIVNY-HLDR-FRESLTINVQSEPEVTIEGFDGNWYLQRTDVCLKCADANPPATEY | 280 | | |
| | | | | | |
| Qy | 303 | VWRSLDGOWPDGLLASDNTLHFVHPLTFNTSYGYICKVTKNSLGORSOKVIYISDPPTTT | 362 | | |
| Dd | 281 | HWTTLGSLPKGVEAQNRLLTFRRGIPTVYSLAGTYICEBATNPIGTRSQGEVNIFFPYTP | 340 | | |
| | | | | | |
| Qy | 363 | TLOPTIQWPSTADIEDLATEPKKLPPPLSTLATIKODTIATIIASVVGALFVLVSVL | 422 | | |
| Dd | 341 | TPE-----HGRRAG-----OMP-----TAIGGVAGSVLLVLI-VV | 370 | | |
| | | | | | |
| Qy | 423 | AGIF--CYRRRTFRGDYFAKNYI-----PPSDMQESQIDVLQOEDLSY | 466 | | |
| Dd | 371 | GGIIVALLRRRRHTFKGDYSTKKHYGNGYSKAGIPQHHP--NAQLNQ-----Y | 417 | | |
| | | | | | |
| Qy | 467 | PDSVKKENK-NPVNNILRKDYLEEPEKTQNNVE-----NLNRFER | 506 | | |
| Dd | 418 | PDDSDEKKAGPLGG---SSSYEEEEEEGGGGGKRVGPHPKYDEDAKPFTYVDAEA | 474 | | |
| | | | | | |
| Qy | 507 | PMDYEDLKMGKFVSDHEHDENEDDLVSHVDGSVISRREYV | 549 | | |
| Dd | 475 | RQGYGDRTLGYQY--DPEQLDLAENVMSQNDGSFISKKEYYV | 515 | | |
| | | | | | |
| RESULT 12 | | | | | |
| PVRL_HUMAN | | | | | |
| ID_PVRL_HUMAN | STANDARD; | PRT; | 517 | AA. | |
| AC | Q15223; O7S465; Q9HB66; Q9HBW2; | | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | | |


```
Best Local Similarity 31.9%; Pred. No. 7.8e-40;
Matches 167; Conservative 80; Mismatches 182; Indels 95; Gaps 17;

Qy 71 GKNVSLKCLIE--VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 127
Dy 44 GTDVLVHCSFANPLPVKTIQVTKQSTNGSKQNVAIYNPMSGVSLAPYRVERFLRPS 103
Qy 128 LNDATITLHNGFSDSGKGYKICAVTFPLGNAQSTTVTLVPTVSLIKGPDSLDG--- 184
Dy 104 FTDGTRLSRLEDEGEVYICEFATPTTGNRESQNLNLTWMAKPT-NWIEGTQAVLRAKKG 162
Qy 185 -GNETVAAICAAATGKPAHIDWEGDL-GEMESTTSPNETATISQYKLPFRFARGR 242
Dy 163 QDDKVLVATCTSANGKPPSVSWETRLKGEABYQIRNPNGTIVISRYLVPBREAHQQ 222
Qy 243 RITCVKHPALEKDIRYSFILDIOVAPEVSVTYGDGNFVGRKGVNLCNADANPPPPFKS 302
Dy 223 SLACIVNYHM--DRFKESLTINVQYEPVETIEGFDGNWYLMQMDVKLTCKADANPPATEY 280
Qy 303 VWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQSGDSQKVIYISDPPTTT 362
Dy 281 HWTTLNGLSLPKGVQAQNRITLFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYT- 339
Qy 363 TLQPTIQHPSTADIEDLATEPKLPPLSLATIKODTITATIASVVGGLFVLVSVL 422
Dy 340 ---PSPPEHGRAG-----PVP-----TAITGGVAGSILLVLI-VV 371
Qy 423 AGIF--CYRRRTFRGDFYAKNYI-----PPSDMOKESQIDVLQDELDSY 466
Dy 372 GGIIVVALRRRHTFKGDYSTKHYVNGYSGKAGIPQHHPP--MAQNLQ-----Y 418
Qy 467 PDSVKKENK-NPVNVLIRKQVLEPEKTQWN-----VENLARFE 505
Dy 419 PDSDEKKAGPLGG---SSYESESEEGGGERKVGPHKPYDEDAKRPYTVDEAE 475
Qy 506 RPDYDDELKMGKFPVSDHEDNEDDLVSHVDSGVSIRREWYV 549
Dy 476 ARQDGYGDRTLGYQY--DPEQLDAENMVNSQDGSFISKKEWYV 517

RESULT 13
PVRL_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HveC) (Nectin 1).
GN Name=PVRL1; Synonyms=HVEC, PRR1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RL is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
CC -!- FUNCTION: Probably involved in cell adhesion. Receptor for
CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
CC cells.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
EMBL: AF308632; AAC30281.1; -.
HSSP: Q05793; IGL4
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
KW Signal; transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 515 Poliovirus receptor related protein 1.
FT DOMAIN 31 355 Extracellular (Potential).
FT TRANSMEM 356 376 Potential.
FT DOMAIN 377 515 Cytoplasmic (Potential).
FT DOMAIN 31 141 Ig-like V-type.
FT DOMAIN 145 243 Ig-like C2-type 1.
FT DOMAIN 247 334 Ig-like C2-type 2.
FT DOMAIN 437 443 Poly-Glu.
FT DOMAIN 444 447 Poly-Gly.
FT DISULFID 51 124 By similarity.
FT DISULFID 172 226 By similarity.
FT DISULFID 269 316 By similarity.
FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 286 286 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 332 332 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDDE3785 CRC64;

Query Match 22.1%; Score 641.5; DB 1; Length 515;
Best Local Similarity 32.0%; Pred. No. 3.1e-39;
Matches 170; Conservative 85; Mismatches 202; Indels 75; Gaps 17;

Qy 52 LCGALAGPIIVEPHVTAVWGNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQ 108
Dy 25 LPGAHTQVQVNDMSYGFIGTDVVLHCSFANPLPGVKITQVTKQSTNGSKQNVAIYNP 84
Qy 109 YGFSVQGEYQGRVLFKNYSLNDATITLHNGFSDSGKGYKICAVTFPLGNAQSTTVTLV 168
Dy 85 MGVSVLAPYRVERFLRPSFTDGTIRLSRLEDEGEVYICEFATFPAGNRESQNLNLTWA 144
Qy 169 EPTVSLIKGPDSLDG---GNETVAAICAAATGKPAHIDWEGDL-GEMESTTSPFNE 223
Dy 145 KPT-NWIEGTQAVLRAKKGDDKVLVATCTSANGKPPSVSWETHLKGABYQIRNPNG 203
Qy 224 TATISQYKLPFRFARGRITCVVHHPALEKDIRYSFILDIOVAPEVSVTYGDGNWYV 283
Dy 204 TTVTISRRLVPSREDHRSQSLACTVNYHM--DRFESLTINVQYEPVETIEGFDGNWY 261
Qy 284 RKGYNLCNADANPPPKFSVWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVNTS 343
Dy 262 RMDVKLTCKADANPPATEYHWTTLNGLSLPKGVQAQNRITLFKGPINYSLAGTYICEATNP 321
Qy 344 LQGRSDQKVIYISDPPTTTTLQPTIQHPSTADIEDLATEPKLPPLSLATIKODTIA 403
Dy 322 IGTRSGQVEVNITEFPYT---PSPPEHGRAG-----QVP-----T 354
Qy 404 TITASVVGGLFVLVSVLAGI---FCYRRRTFRGDFYAKNYI-----PP 446
Dy 355 AIIGWVGSIILLVLF--VVGIVVALC-RRRHTFKGDYSTKHYVNGYSGKAGIPQHHPP 411
Qy 447 SDMQESQIDVLQDELDSYP---DSVKENKQNPVNLIRK-----DYLEEPEKTQWN 497
Dy 412 --MAQNLQYPEDSDDEKKAGPLGGSSYESESEEGGGERKVGPHKPYDEDAKRPYF-- 467
```


RT "Complete sequencing and characterization of 21,243 full-length human

```
CDNAS." ;
RT      NAT. Genet. 36:40-45(2004).
RL      EMBL; AK027753; BAB55344.1; -.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003598; IG_C2.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00408; IGC2; 1.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      Receptor.
KW      SEQUENCE.
SQ      510 AA; 55382 MW; 9868CD50F086429E CRC64;
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Search completed: October 6, 2005, 10:19:36
Job time : 85.4368 secs

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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 22.9914 Seconds
(without alignments)
1782.508 Million cell updates/sec

Title: US-09-972-268-4
Perfect score: 2905
Sequence: 1 MATPGSPCLPGGGKAQLS.....EDDLVSHVDSVSRREWYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 649.5 | 22.4 | 514 | 4 | US-09-949-016-11380 |
| 2 | 649.5 | 22.4 | 514 | 4 | US-09-723-368-4 |
| 3 | 627 | 21.6 | 518 | 4 | US-09-919-172-20 |
| 4 | 566 | 19.5 | 458 | 4 | US-09-435-956A-1 |
| 5 | 472 | 16.2 | 522 | 4 | US-09-949-016-7563 |
| 6 | 463 | 15.9 | 479 | 4 | US-09-723-368-2 |
| 7 | 463 | 15.9 | 479 | 4 | US-09-949-016-6278 |
| 8 | 397.5 | 13.7 | 456 | 4 | US-09-949-016-7564 |
| 9 | 391 | 13.5 | 408 | 3 | US-09-724-864-62 |
| 10 | 390.5 | 13.4 | 417 | 4 | US-09-949-016-6729 |
| 11 | 335.5 | 11.5 | 442 | 4 | US-09-778-510-20 |
| 12 | 335.5 | 11.5 | 442 | 4 | US-09-930-803-1 |
| 13 | 333.5 | 11.5 | 440 | 4 | US-09-866-028-61 |
| 14 | 333.5 | 11.5 | 440 | 4 | US-09-944-457-61 |
| 15 | 325.5 | 11.2 | 423 | 4 | US-09-778-510-22 |
| 16 | 263 | 9.1 | 444 | 2 | US-08-659-984A-5 |
| 17 | 263 | 9.1 | 444 | 3 | US-08-660-531-5 |
| 18 | 255.5 | 8.8 | 421 | 2 | US-08-659-984A-1 |
| 19 | 255.5 | 8.8 | 421 | 3 | US-08-660-531-1 |
| 20 | 249 | 8.6 | 398 | 4 | US-09-778-510-4 |
| 21 | 243 | 8.4 | 398 | 4 | US-09-778-510-6 |
| 22 | 243 | 8.4 | 398 | 4 | US-09-907-794A-84 |
| 23 | 243 | 8.4 | 398 | 4 | US-09-905-125A-84 |
| 24 | 243 | 8.4 | 398 | 4 | US-09-902-775A-84 |
| 25 | 243 | 8.4 | 398 | 4 | US-09-906-700-84 |
| 26 | 243 | 8.4 | 398 | 4 | US-09-903-603A-84 |
| 27 | 243 | 8.4 | 398 | 4 | US-09-904-920A-84 |

| | | | | | | |
|----|-------|-----|------|---|---------------------|-------------------|
| 28 | 243 | 8.4 | 398 | 4 | US-09-909-064-84 | Sequence 84, Appl |
| 29 | 243 | 8.4 | 398 | 4 | US-09-905-381A-84 | Sequence 84, Appl |
| 30 | 243 | 8.4 | 398 | 4 | US-09-906-618-84 | Sequence 84, Appl |
| 31 | 233 | 8.0 | 432 | 4 | US-09-778-510-2 | Sequence 2, Appl |
| 32 | 215.5 | 7.4 | 4391 | 4 | US-10-006-011A-2 | Sequence 2, Appl |
| 33 | 190.5 | 6.6 | 227 | 4 | US-09-205-258-947 | Sequence 947, App |
| 34 | 189.5 | 6.5 | 837 | 4 | US-09-949-016-6515 | Sequence 6515, Ap |
| 35 | 187.5 | 6.5 | 274 | 3 | US-09-570-367C-19 | Sequence 19, Appl |
| 36 | 187.5 | 6.5 | 274 | 4 | US-09-915-524-19 | Sequence 19, Appl |
| 37 | 187.5 | 6.5 | 274 | 4 | US-09-934-634-19 | Sequence 19, Appl |
| 38 | 182.5 | 6.3 | 819 | 4 | US-09-949-016-11044 | Sequence 11044, A |
| 39 | 173.5 | 6.0 | 588 | 4 | US-09-949-016-10547 | Sequence 10547, A |
| 40 | 169 | 5.8 | 626 | 4 | US-09-949-016-6213 | Sequence 6213, Ap |
| 41 | 169 | 5.8 | 664 | 4 | US-09-949-016-7850 | Sequence 7850, Ap |
| 42 | 167.5 | 5.8 | 1709 | 4 | US-09-949-016-10503 | Sequence 10503, A |
| 43 | 166 | 5.7 | 1101 | 3 | US-08-986-485-2 | Sequence 2, Appl |
| 44 | 164 | 5.6 | 477 | 2 | US-08-432-016-3 | Sequence 3, Appl |
| 45 | 164 | 5.6 | 477 | 2 | US-08-684-594-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1

US-09-949-016-11380
; Sequence 11380, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11380
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11380

| | | | | | |
|-----------------------|-----|---|---|------------|-------------|
| Query Match | | 22.4% | Score 649.5; | DB 4; | Length 514; |
| Best Local Similarity | | 31.9%; | Pred. No. 2.4e-51; | | |
| Matches 167; | | Conservative 80; | Mismatches 182; | Indels 95; | Gaps 17; |
| Qy | 71 | GKNVSLKCLIE--- | VNETITQISWEKTHGKSSQTVAVHHPOYGFSGVEYQGRVLFKNYS | 127 | |
| Db | 41 | GTDVLLHCSFANPLPSVKIIQVTQWQKSTNGSKQNVAINFSGMVSUAPYRVERFLRPS | 100 | | |
| Qy | 128 | LNDAITILHNIIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGDSLDG--- | 184 | | |
| Db | 101 | FTDGTIRLSRLELEDEGVICEFATFTGNRESQLNLTVMAKPT-NWIEGTQAVLRKKG | 159 | | |
| Qy | 185 | -GNETVAACIAATGKPVAHIDWEGDL-GEMESTTTFSPNETATIIIOYKLPFTRFARGR | 242 | | |
| Db | 160 | QDDKVLVATCISANGKPPSVVSWETRLKGEAEYQIEIRNPNGTIVTVISRYRLVPSREAHQ | 219 | | |
| Qy | 243 | RITCVKHPALEKDIRYSFILDIOYAPEVSUTGVDGNWFCVRKGVNLCNADANPPPKS | 302 | | |
| Db | 220 | SLACIVNHYM--DRFKESLTINVQYEPETIEGPDGNWYLQRMVMDVKLTCKADANPPATEY | 277 | | |
| Qy | 303 | VWSRLDGQWPDGLIASDNTLHFVHPLTFNYSGVICKVNTSLGORSQKVIYISDPPTTT | 362 | | |
| Db | 278 | HWTTLNLSLPGVEAQNRTLFFKGPINYSLAGTYICATNPIGTRSGQVEVNIETFPYT- | 336 | | |
| Qy | 363 | TLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDITATIATIASVVGALFIVLVSVL | 422 | | |

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Db 337 ---PSPPEHGRAG-----PVP-----TAIIGVAGSILLVLI-VV 368
QY 423 AGIF--CYRRRTFRGDFYFAKNYI-----PPSDMKESQIDVLQDDELDSY 466
Db 369 GGIWVALRRRRTFKGDTSTKHHVNGYSGKAGIPOHHPP--MAQNLQ-----Y 415
QY 467 PDSVKKENK-NPVNNLIRKDYLEPEKTOAWN-----VENLNRFE 505
Db 416 PDSDDKAGPLGG---SSYEEREEEGGGGERKVGPHPKYDEDAKRPYFTVDEAE 472
QY 506 RPDYEDYDLKMGKMFVSDHYDENEDDLVSHVDGVSISRREWTV 549
Db 473 ARQDGYGDRTLGYQY--DPEQLDLAENMVSNQDGSFISKKEWTV 514
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RESULT 2

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US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/201
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4
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Query Match 22.4%; Score 649.5; DB 4; Length 517;
Best Local Similarity 31.9%; Pred. No. 2.4e-51;
Matches 167; Conservative 80; Mismatches 182; Indels 95; Gaps 17;

QY 71 GKNSVSLKCLIE---VNETITQISWEKHGKSSQTVAVHHFPQYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNSMGVSVLAPYRERVEFLRPS 103

QY 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVLSIKGPDLSLDG--- 184
Db 104 FTDGTIRLSRLEDEGVYICEFATFTGNRESQNLNTVMAKPT--NWIETGQAVLRAKKG 162

QY 185 -GNETVAACIAATGKPVAHIDWEGDL--GEMESTTTSPNETATIIISOYKLPPTFRAGR 242
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAYQEIERNPNGVTIVISRYRLVPSREAHQQ 222

QY 243 RITCWVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVRGKGNLKNADANPPPFKS 302
Db 223 SLACIVNYHM--DRFKESLTLNVQYEPETVIEGFGNNWYLRQMDVKLTCKADANPPATEY 280

QY 303 VWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVVICKVTSLSGORSQKVIYISDPPTTT 362
Db 281 HWTTLNGLSLPKGVEAQRNTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNIIEFPYT- 339

QY 363 TLQPTIQWHPSTADIEDLATEPKKLPFPLSLATIKDPTIATIIASVVGALFVLVSVL 422
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Db 340 ---PSPPEHGRAG-----PVP-----TAIIGVAGSILLVLI-VV 371
QY 423 AGIF--CYRRRTFRGDFYFAKNYI-----PPSDMKESQIDVLQDDELDSY 466
Db 372 GGIWVALRRRRTFKGDTSTKHHVNGYSGKAGIPOHHPP--MAQNLQ-----Y 418
QY 467 PDSVKKENK-NPVNNLIRKDYLEPEKTOAWN-----VENLNRFE 505
Db 419 PDSDDKAGPLGG---SSYEEREEEGGGGERKVGPHPKYDEDAKRPYFTVDEAE 475
QY 506 RPDYEDYDLKMGKMFVSDHYDENEDDLVSHVDGVSISRREWTV 549
Db 476 ARQDGYGDRTLGYQY--DPEQLDLAENMVSNQDGSFISKKEWTV 517

RESULT 3
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20
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Query Match 21.6%; Score 627; DB 4; Length 518;
Best Local Similarity 30.8%; Pred. No. 3e-49;
Matches 164; Conservative 80; Mismatches 177; Indels 112; Gaps 18;

QY 71 GKNSVSLKCLIE---VNETITQISWEKHGKSSQTVAVHHFPQYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNSMGVSVLAPYRERVEFLRPS 103

QY 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVLSIKGPDLSLDG--- 184
Db 104 FTDGTIRLSRLEDEGVYICEFATFTGNRESQNLNTVMAKPT--NWIETGQAVLRAKKG 162

QY 185 -GNETVAACIAATGKPVAHIDWEGDL--GEMESTTTSPNETATIIISOYKLPPTFRAGR 233
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAYQEIERNPNGVTIVISRYRLVPSREAHQQ 214

QY 234 FPTFRAGRRTICVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVRGKGNLKNADAN 293
Db 215 VPSREAHQQSLACIVNYHM--DRFKESLTLNVQYEPETVIEGFGNNWYLRQMDVKLTCKA 272

QY 294 DANPPPFKS VWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVVICKVTSLSGORSQKVI 353
Db 273 DANPPATEYHWTTLNGLSLPKGVEAQRNTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332

QY 354 YISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSLATIKDPTIATIIASVVGGA 413
Db 333 NITEFPYT---FSPPEHGRAG-----PVP-----TAIIGVAGS 364

QY 414 LFIVLSVLGAGIF--CYRRRTFRGDFYFAKNYI-----PPSDMKESQIDV 457
Db 365 ILLVLI-VWGGIVVALRRRRTFKGDTSTKHHVNGYSGKAGIPOHHPP--MAQNLQ----- 418

QY 458 LQDDELDSYDPSVKKENK-NPVNNLIRKDYLEPEKTOAWN----- 497
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Db 419 -----YPPDSDEKXAGPLGG---SSVEEBEEDGGGGGKRGKVGHPKPYDEDAKR 467
Qy 498 -VENLNFRPMYDYEDLKMGMKFSVDEHYDNEEDDLVSHVDGSGVISRRWYV 549
Db 468 PYFTVDBAEARQDGYGDRTLGYQY--DPEQLDAENNVNQDGSFISKWKYV 518

RESULT 4
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; TITLE OF INVENTION: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 19.5%; Score 566; DB 4; Length 458;
Best Local Similarity 31.3%; Pred. No. 1.1e-43;
Matches 141; Conservative 75; Mismatches 169; Indels 66; Gaps 12;

Qy 71 GKNSLKLIE--VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYGRVLFKNYS 127
Db 44 GTDVLHCSFANPLSPVKITQVTKSTNGSKQNVAIYNSMGVSLAPYRVERVEFLRPS 103
Qy 128 LNDATITLHNIQFSDSGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPDSLIDG--- 184
Db 104 FTDGTIRLSRLEDEGVYICGFATFPNGNRESQNLNLTVMKPT-NWIEGTQAVLRKKG 162
Qy 185 -GNETVAACIAATGKPVAHIDWEGDL-GENESTTTSPNETATIIISQYKLPFTRFARGR 242
Db 163 QDDKVLVATCTSANGKPPSVSVSWETRLKGEAEYQBIIRPNGTVTIVISRYRLVPSREAHQ 222
Qy 243 RITCVKHPALEKDIRYSFILDIOYAPRSVTVGVDGNWFCRGKGNLKNADANPPPKS 302
Db 223 SLACIVNYHM--DRFKESLTINQVPEVTTEGGDGNLYLQMDVKLTCKADANPPATEY 280
Qy 303 VWSRLDGQWPGLLASDNTLHFVHPLTENYSGVICKVNSLQORSQDKYIISDPPTTT 362
Db 281 HWTTLNGLPKGVEAQNRTLFKGPINSLAGTICENTNIGTRSGQVEVNIETKEP-- 338
Qy 363 TLQPTIQWHPSTADIEDLATEPKLPPFLSTLATIKDPTIATIIASVVGGLFVLVSVL 422
Db 339 -----PQRLG-----SAARLLAGTV--AVFLILVAVL 364
Qy 423 AGIFCYRRRTFRGDFYAKNVIIPSDMOKESQIDVLQODE-LDSYDPSVKKNKPNVNL 481
Db 365 TVFFLYNRQK-----SPP-----ETDAGTDQPLSQKPEPSRQSSLVED 407
Qy 482 IRKDYLEPEKTOQNNVNENLNRFRPMDYYE 512
Qy 408 IQVHVL-DPGRQQQEEEDLQKLSLPYYD 437

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RESULT 5
US-09-949-016-7563
; Sequence 7563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7563
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7563

Query Match 16.2%; Score 472; DB 4; Length 522;
Best Local Similarity 25.5%; Pred. No. 7.4e-35;
Matches 155; Conservative 79; Mismatches 204; Indels 170; Gaps 21;

Qy 3 RTPGSPCLPGGKAQLSSASLLGAGLL--LQPPTPPPLLLLPPLLLFSRL-CCALAGP 59
Db 24 RPQSGPRAGRAQSPGPGPMARAAALLPSPPTP-----LLWPLLLLLLETGAQDVR 78
Qy 60 IIVEPHVTAVMGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPOYGFVSQ 115
Db 79 QVQLPEVRGQLGGTVLPCHLLPPVPGLYISLVTWQRPDAPANNQNVAAAFPKMGSPSPS 138
Qy 116 EYQG--RVLF-----KNYSLNDATITLHNIQFSDSGKYICKAVTFPLGNAQSSTT 163
Db 139 PKPGSERLSFSAKQSTQGTAELODATALHGLTVEDEGNYTCEFATFPKPSVRGMTW 198
Qy 164 VTVLVEP-----TVSLIKGPDSLIDGNETVAAICIAATGKPAVHT-----DWEGDL 210
Db 199 LRVIAKPKNOAEAKQVTFSDQD-----TTVALCISKEGRPPARISWLSLDEAKE 249
Qy 211 GEMESTTTSPNETATIIISQYKLPFTRFARGRRITCVVGHKPALEKDIRYSFILDIOYAPE 270
Db 250 TVSGTLAG---TVTVTSRFTLVPSGRADGVTVTKVEHESFEPEPALIPVTLVRYPE 305
Qy 271 VSVTGYDGNWFCRGKGNLKNADANPPPKSVMSRLDGQWPGDGLLASDNTLHFVHPLTF 330
Db 306 VVISGYDDNWYLGRTDATALSCDVRSNPEPTGYDWSSTTSGTPTSAVAGSQL-VIHA VDS 364
Qy 331 NYSGVYICKVNSLQORSQDKYIISDPPTTTTLOPTIQWHPSTADIEDLATEPKLPPFP 390
Db 365 LFNFTFTVTVTVNMGRAEQVIFVRETPT----- 394
Qy 391 LSTLATIKDPTIATIIASVVGGLFVLVSVLAG-----IFCYRRRTF----- 434
Db 395 -----ASPRD--VGPLWVGAVGGTLLVLL--LLAGSLAFILLRVRRRRKSFGGAGGASG 446
Qy 435 -----RGDYFAKNYIPPSDMOKESQIDVLQODELDSYDPSVKKNKPNVNL 481
Db 447 DGGFYDPKAVLGNQDPVFVTFPVVPGPME-----PDG----- 478
Qy 482 IRKDYLEPEKTOQNNVNENLNRFRPMDYYEDLKMGMKFSVDEHYDNEEDDLVSHVDG 541
Db 479 --KDEEBEES-----EKAEGKGLMLPPPPAL---EDDMESQLDGLS 514
Qy 542 ISREWYV 549
Db 515 ISRRAYV 522

```

RESULT 6
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 15.9%; Score 463; DB 4; Length 479;
Best Local Similarity 25.7%; Pred. No. 4.4e-34;
Matches 148; Conservative 76; Mismatches 184; Indels 168; Gaps 20;

QY 33 PPTPPPLLLLFPPLLSRL-CCALAGPIIVEHPTVAVMKVNSLKLI---EVNETITQ 88
DB 13 PPTP-----LLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVLPCPLLPPVGLYISL 67

QY 89 ISWEKIHGSS-QTVAVHHPOYGFVSQGEYQG--RVLF-----KNYSINDATITL 135
DB 68 VTWQRPDAPANHQNVAFAHFKMGSPSPKPGSERLSFVSAKOSTQDTEAEIQLDATAL 127

QY 136 HNTGFSDSGKICKAVTFFPLGNAQSSTTVTLVLEP-----TVSLIKGPDSLIDGNET 188
DB 128 HGLTVEDEGNYTCEFAFPFKGSRGVTWLRVIAPKNQAEAKVTFSDP-----T 178

QY 189 VAAICIAATKGPVAHI-----DWEDLGEMESTTTSFPNETATIIISOYKLFPTFRFARGR 242
DB 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG-----TVTVTSRFTLVPSGRADGV 234

QY 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVGTGDNWFGVRKGVNLCNADANPPFPKS 302
DB 235 TVTCKVEHESFEERPALIPVTLVRYPEVSISGYDDNWYLGRTDATALSCDVRNPEPTY 294

QY 303 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTT 362
DB 295 DWSTTSGTFTSAVAQSQL-VIHAVDSLNTFVCTVTNAVGMRAEQVIFVRETPR-- 351

QY 363 TLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFVLVSVL 422
DB 352 -----ASPRD--VGPLVWGAVGGLTLVLL--LL 375

QY 423 AG-----IFCYRRRTTF-----RGDYFAKNYIPPSDMOKES 453
DB 376 AGGSLAFILLRVRRRRKSPGAGGASGGGDFYDPAQVLGNGDPVFWTVPVPGPME--- 432

QY 454 QIDVLOQDELSDYSPDKENKNPNVNLIRKDYLEBEPEKTMNNVENLNFRFPMYD 513
DB 433 -----PDG-----KDEEEEEE-----EK 446

QY 514 LKMGKMFVSDHEHYDENEDDLVSHVDGVSISRREWYV 549
DB 447 AEKGLMLPPPPAL---EDDMESQLDGLSLISRRAVYV 479

RESULT 7
US-09-949-016-6278
; Sequence 6278, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6278
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6278

Query Match 15.9%; Score 463; DB 4; Length 479;
Best Local Similarity 25.7%; Pred. No. 4.4e-34;
Matches 148; Conservative 76; Mismatches 184; Indels 168; Gaps 20;

QY 33 PPTPPPLLLLFPPLLSRL-CCALAGPIIVEHPTVAVMKVNSLKLI---EVNETITQ 88
DB 13 PPTP-----LLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVLPCPLLPPVGLYISL 67

QY 89 ISWEKIHGSS-QTVAVHHPOYGFVSQGEYQG--RVLF-----KNYSINDATITL 135
DB 68 VTWQRPDAPANHQNVAFAHFKMGSPSPKPGSERLSFVSAKOSTQDTEAEIQLDATAL 127

QY 136 HNTGFSDSGKICKAVTFFPLGNAQSSTTVTLVLEP-----TVSLIKGPDSLIDGNET 188
DB 128 HGLTVEDEGNYTCEFAFPFKGSRGVTWLRVIAPKNQAEAKVTFSDP-----T 178

QY 189 VAAICIAATKGPVAHI-----DWEDLGEMESTTTSFPNETATIIISOYKLFPTFRFARGR 242
DB 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG-----TVTVTSRFTLVPSGRADGV 234

QY 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVGTGDNWFGVRKGVNLCNADANPPFPKS 302
DB 235 TVTCKVEHESFEERPALIPVTLVRYPEVSISGYDDNWYLGRTDATALSCDVRNPEPTY 294

QY 303 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTT 362
DB 295 DWSTTSGTFTSAVAQSQL-VIHAVDSLNTFVCTVTNAVGMRAEQVIFVRETPR-- 351

QY 363 TLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFVLVSVL 422
DB 352 -----ASPRD--VGPLVWGAVGGLTLVLL--LL 375

QY 423 AG-----IFCYRRRTTF-----RGDYFAKNYIPPSDMOKES 453
DB 376 AGGSLAFILLRVRRRRKSPGAGGASGGGDFYDPAQVLGNGDPVFWTVPVPGPME--- 432

QY 454 QIDVLOQDELSDYSPDKENKNPNVNLIRKDYLEBEPEKTMNNVENLNFRFPMYD 513
DB 433 -----PDG-----KDEEEEEE-----EK 446

RESULT 8

US-09-949-016-7564
; Sequence 7564, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7564
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7564

Query Match 13.7%; Score 397.5; DB 4; Length 456;
Best Local Similarity 26.9%; Pred. No. 4.9e-28;
Matches 124; Conservative 71; Mismatches 183; Indels 83; Gaps 16;
Qy 4 TPGSPCLPGG-----GKA-----QLSSASLGA-GLLLQPTPPPLL 40
Db 21 TPGTGGAAPGFDLSSGSTRSRGRASWRERARRPREQLLGATGARAMAAWPLL 80
Qy 41 LLLPFLFLSRLCAGAPIIVE--PHVTAVGKNVSLKCLIEVNET----ITQISWEKI 94
Db 81 LVALLVLVSWP---PPGTGDDVVQAPTQVPGFLGDSVTLPCVLPVNMETHVSQLTWAR- 136
Qy 95 HGKSSQTVAVH---POYGFVSQGEYQGRVLFKNYSLNDAITILHNTGFSQSGKYICKAV 151
Db 137 HGESGMAVFHOTQGPSYSESKLEFVAARL--GAELRNASLRMFLGRVEDEGNYTCLFV 194
Qy 152 TPLPNAQSSSTTVTLVLEP--TVSLIKGPDSDILGNETVAACIAATGKPVAHIDWEGD 209
Db 195 TFPQSGRSVDILWRLAKPQNTAEVQVKQLT---GEPPVMARCVSTGGRPPAQITWHD 250
Qy 210 LGEMESTT--TSFPNETATILSQYKLPRTFARGRRITCVVKHPALEKDIIYSFILDIOY 267
Db 251 LGGMPTSQVPGFUSGTVTSLMLVPSSQVDGKNVTCRVEHSEFKPQLLTVNLVYV 310
Qy 268 APEVSVTGYDGNFVGRGVNKLKNADANPPFPKSVMSRLDGQWPDGILLASDNTLHFVHP 327
Db 311 PPEVSIQYDNNWYLGQNEATLTCDARSNPETGYNWSTMGPLPPFAVAQAGL-LIRP 369
Qy 328 LTFNYSYVICKTNSLQGRSDQKVIYISDPTTTTLQPTIQWHPSTADIEDLATEPKKL 387
Db 370 VDKPINTTLCNVNTNALGARQAEITVQKEGP----- 401
Qy 388 PFPLSTLATIKDDTIATIIASVVGALFIVLVSVLGIFCY 428
Db 402 PSEHSGMSR-----NAIFIVLVLGILVPLILLGI--GIYFY 434

RESULT 9

US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; by the polynucleotides and methods for their use.

FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match 13.5%; Score 391; DB 3; Length 408;
Best Local Similarity 28.0%; Pred. No. 1.6e-27;
Matches 134; Conservative 71; Mismatches 178; Indels 96; Gaps 19;
Qy 17 AOLSSASLLGAGLLQPTPPPPPLLLLLLFPPLLSRLCGAL--AG---PIIVEPHVTAVWG 71
Db 2 AQLARAT-----RSPLSWLLLF-----CYALRKAGGDIRLVFPYNSTGVLG 43
Qy 72 KNYSLKCLIEVNE--TITQISW-EKIHGKSQTVAVHHPOYGFVSQGEYQGRVLFKNVSL 128
Db 44 GSTTLHCSLTSNENVTITQITMMKDSGSHALVAVFHPKGPNIKPERVKFLAAQODL 103
Qy 129 NDATITLHNTGFSQSGKYICKAVTFFPLGNAQSSSTTVTLVLEP--TVSLIKGPDSDLI--DG 184
Db 104 RNASLAISNLSVEDEGIYEQIATFFRGSSTNAWLKVQAPKNTAEALSPSTLILQD- 162
Qy 185 GNETVAAICIAATGKPVAHIDW-----EGDLEGEMSTTTSPNETATIIISQYKLPPTPAR 240
Db 163 -----VAKCISANGHPGGRISWPSNVNGSHREMKP-PSQPG-TTTVTLSLWVPSRQAD 215
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOVAPE-VSVTGDGWNFVGRGVNKLKNADANPPP 299
Db 216 GKNITCTVHESLQELDQLLVLTLSQYPPENVSISYDGNWYVGLTNLTLTCEAHSKPAP 275
Qy 300 FKS--VMSRLDGQWPDGILLASDNTLHFVHPITFNYSYVICKTNSLQGRSDQKVIYISD 357
Db 276 DMAGYNNSTNGTGFNFNSVKRGNNMLLISTVEDGLNNTVIVCEVTNALSGGGQVHHIIVKE 335
Qy 358 PPTTTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIV 417
Db 336 KP--ENMQQNTRLHL----- 354
Qy 418 -----LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLOQDELDSYDVK 471
Db 355 VFVLAVVIIIAALYTIIRRCR--HGRALQSN---PSERENQYSSVNGDCRLNMEPNSTR 408

RESULT 10

US-09-949-016-6729
; Sequence 6729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6729
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human

US-09-949-016-6729

Query Match 13.4%; Score 390.5; DB 4; Length 417;
Best Local Similarity 27.6%; Pred. No. 1.9e-27;
Matches 111; Conservative 68; Mismatches 162; Indels 61; Gaps 13;
QY 44 FPLLLSRLCGAL-----AGPIIVE--PHVTAVMGKNVSLKCLIEVNET-----ITQISWEK 93
DB 9 WPLLLVALLVLSWPPPGCTGDDVQAQTVQVPGFLGDSVTLPCYLQVPMVEVTHVSQLTWIR 68
QY 94 IHKKSQTVAVHH---POYGFSVOGEGQKRVLPKNVSLNDATITLHNGFSDSGKYICKA 150
DB 69 -HGEGSMVAFHQTCQPSYSESKRLFEVAARL--GAELRNASLRMFGLRVEDEGNTCLF 125
QY 151 VTEPLGNAQSSVTVLVEP--TVSLIKGPDSDLIDGNETVAICIAATKPKVAHIDWEG 208
DB 126 VTFPQSRSDIWLRLVLAQPNTAEQVKQVLT---GEPVPMARCVSTGGRPPAQITWHS 181
QY 209 DLGEMESTT--TSFPNETATIIISQYKLFPTFRFARRRITCVVKHPALEKDRIYSFILDIO 266
DB 182 DLGCMNTSQVPGFLSGTVTVTSLWLVPSSQVDGKNVCKVEHSEFEKPOLLTVNLTVY 241
QY 267 YAPEVSVGTGDNFVGRKGNVKNLKNADANPPPKFSVMSRLDGOWPDGLLASDNTLHFVH 326
DB 242 YPEVSGISGDDNNWYLQNEATLTCDAARSNEPTGYNMWSTMGPLPPFAVQAQAL-LIR 300
QY 327 PLTFNYSGVVICKVNTSLGORSQKVIYISDPPTTTTTLQPTIOHHPSTADIEDLATEPKK 386
DB 301 PVDKPINTLLCNVTNALGARQAEITVQKEGP----- 333
QY 387 LPFPLSLATIKDOTTIATIASVVGALFVLVSLAGIFCY 428
DB 334 -PSEHSGMSR-----NAILFLVLGILVFLILGI--GIYFY 366

RESULT 11

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

Query Match 11.5%; Score 335.5; DB 4; Length 442;
Best Local Similarity 25.5%; Pred. No. 2.7e-22;
Matches 115; Conservative 87; Mismatches 182; Indels 67; Gaps 18;
QY 8 SPLCPGGKQAQLSASLLGAGLLLOPTPPPLLLLLLFPRLCGALAGPIIIVPHVT 67
DB 3 SVVLPSSQCAAAAAPPLRLR-----LILLFSA---AALPTGQGNLFTKDVT 53
QY 68 AVGKNVSLKCLIEVNETITQISWEKIHGKSSOTVAVHHPOYGFSVOGEGQKRVLPKNYS 127
DB 54 VIEGEVATISC--QVKNSSDSVI--QLLNPNRQTI-----YFRDFPLKDSRFQLNFS 103
US-09-778-510-20

QY 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMESTTTFPNETATIIISQYKLFPTFRAR 240
DB 160 EEIEVNCATAMASKPATITIRWFKGNTLKGKSEVEEWSDMY-----TVTSQMLMKVHKEDD 214
QY 241 GRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGDGNWFVGRKG--VNLKCNADANPP 298
DB 215 GVPVICQVHPHVAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
QY 299 PFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVVICKVNTSLGORSQKVIYISDP 358
DB 275 PVMVTWVRVDDENPQHAVLSGPNL-FINNLTNDNGTYRCEASNIYVKGKASHDYMLVYDP 333
QY 359 PTTTTLQPTIOHHPSTADIEDLATEPKLFPPLSTLATI-----KDDTIATIIASVVG 411
DB 334 P--TTIPP-----PTTTTTTTTT-----TTTILTIITDSRAGEGSIKRAVDHAVIG 378
QY 412 GALFIVLVSLAGIFCYRRRRRTFRGDYFANK 442
DB 379 GVAVVVFVAMLCILLI-----ILGRYFARH 402

RESULT 12

US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHUI770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 11.5%; Score 335.5; DB 4; Length 442;
Best Local Similarity 25.5%; Pred. No. 2.7e-22;
Matches 115; Conservative 87; Mismatches 182; Indels 67; Gaps 18;

QY 8 SPLCPGGKQAQLSASLLGAGLLLOPTPPPLLLLLLFPRLCGALAGPIIIVPHVT 67
DB 3 SVVLPSSQCAAAAAPPLRLR-----LILLFSA---AALPTGQGNLFTKDVT 53
QY 68 AVGKNVSLKCLIEVNETITQISWEKIHGKSSOTVAVHHPOYGFSVOGEGQKRVLPKNYS 127
DB 54 VIEGEVATISC--QVKNSSDSVI--QLLNPNRQTI-----YFRDFPLKDSRFQLNFS 103
QY 128 LNDATITLHNGFSDSGKYICKAVTTPPLGNAQSSVTVLVEPTVSLIK-GPDSLIDGNN 186
DB 104 SSELKVSILTNVISLSDGRYFCQLYTD--POESYTTITVLVPPRNLMDIQTOKTAVEG-- 159
QY 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMESTTTFPNETATIIISQYKLFPTFRAR 240
DB 160 EEIEVNCATAMASKPATITIRWFKGNTLKGKSEVEEWSDMY-----TVTSQMLMKVHKEDD 214
QY 241 GRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGDGNWFVGRKG--VNLKCNADANPP 298
DB 215 GVPVICQVHPHVAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
QY 299 PFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVVICKVNTSLGORSQKVIYISDP 358
DB 275 PVMVTWVRVDDENPQHAVLSGPNL-FINNLTNDNGTYRCEASNIYVKGKASHDYMLVYDP 333
QY 359 PTTTTLQPTIOHHPSTADIEDLATEPKLFPPLSTLATI-----KDDTIATIIASVVG 411
DB 334 P--TTIPP-----PTTTTTTTTT-----TTTILTIITDSRAGEGSIKRAVDHAVIG 378

| | | | | | |
|----|-----|-------------|------------|-----------|-----|
| Qy | 412 | GALFIVLVSVL | AGIFCYRRRT | FRGDYPAKN | 442 |
| | | : : : | : : : | | |
| Db | 379 | GVVAWVFAM | CLLI----- | ILGRYFARH | 402 |

RESULT 13
US-09-866-028-61
; Sequence 61, Application US/09866028

| | | | | |
|---------------------------|-------|------------------|------------|-------------|
| Query Match | 11.5% | Score 333.5; | DB 4; | Length 440; |
| Best Local Similarity | 25.7% | Pred. NO. 4e-22; | | |
| Matches 117; Conservative | 85; | Mismatches 176; | Indels 77; | Gaps 20; |

Db 373 AVIGGVAVVVFAMLCCLI-----ILGRYFARH 400

RESULT 14
US-09-944-457-61

db 1 MARTPGPSPLCPGGGKAOLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSRLCGALAGPI 60

```
QY 61 IVEPHVTAVGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
DB 61 IVEPHVTAVGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
QY 121 VLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
DB 121 VLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
DB 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGDGNWFGVGRKGVNLCNADANPPPF 300
DB 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
DB 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420
DB 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKKENKPNVNN 480
DB 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKKENKPNVNN 480
QY 481 LIRKDYLEEPKTOAWNVENLNRFERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEEPKTOAWNVENLNRFERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
DB 541 VISRREWYV 549
```

RESULT 2

```
US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6
```

```
Query Match 99.4%; Score 2887; DB 10; Length 549;
Best Local Similarity 99.6%; Pred. No. 3.4e-213;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MARTPGSPGPCGGKAQLSSASLLGAGLLLOPPTPPPLLLPPLLLFRLCGALAGPI 60
DB 1 MARTLRSPGPCGGKAQLSSASLLGAGLLLOPPTPPPLLLPPLLLFRLCGALAGPI 60
QY 61 IVEPHVTAVGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
DB 61 IVEPHVTAVGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
```

```
QY 121 VLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
DB 121 VLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
DB 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGDGNWFGVGRKGVNLCNADANPPPF 300
DB 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
DB 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420
DB 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKKENKPNVNN 480
DB 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKKENKPNVNN 480
QY 481 LIRKDYLEEPKTOAWNVENLNRFERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEEPKTOAWNVENLNRFERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
DB 541 VISRREWYV 549
```

RESULT 3

```
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45
```

```
Query Match 99.4%; Score 2887; DB 14; Length 549;
Best Local Similarity 99.6%; Pred. No. 3.4e-213;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 MARTPGSPGPCGGKAQLSSASLLGAGLLLOPPTPPPLLLPPLLLFRLCGALAGPI 60
DB 1 MARTLRSPGPCGGKAQLSSASLLGAGLLLOPPTPPPLLLPPLLLFRLCGALAGPI 60
QY 61 IVEPHVTAVGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
DB 61 IVEPHVTAVGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
```

QY 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPD 180
DB 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPPTFRAR 240
DB 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPPTFRAR 240
QY 241 GRRITCVVHPALEKDIRYFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
DB 241 GRRITCVVHPALEKDIRYFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDPPT 360
DB 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDPPT 360
QY 361 TTTLQPTIOHWPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
DB 361 TTTLQPTIOHWPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
QY 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKNPVNN 480
DB 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKNPVNN 480
QY 481 LIRKDYLEPEKTOVNNVNLNRPFRPMDYYEDLKMGKMFVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEPEKTOVNNVNLNRPFRPMDYYEDLKMGKMFVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
DB 541 VISRREWYV 549

RESULT 4

US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 98.7%; Score 2866; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.4e-211; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPLCPGGKQAQLSASLLGAGLLIQPTPPPLLLPFLLLFSLRCGALAGPIIVEPHVT 67
DB 1 SPLCPGGKQAQLSASLLGAGLLIQPTPPPLLLPFLLLFSLRCGALAGPIIVEPHVT 60
QY 68 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 127
DB 61 AVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 120
QY 128 LNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPD 187
DB 121 LNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPD 180

QY 188 TVAAICIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPPTFRAR 247
DB 181 TVAAICIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPPTFRAR 240
QY 248 VKHPALEKDIRYFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPFKSVMSRL 307
DB 241 VKHPALEKDIRYFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPFKSVMSRL 300
QY 308 DGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDPPTTTTLOPT 367
DB 301 DGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDPPTTTTLOPT 360
QY 368 IQHWPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS 427
DB 361 IQHWPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
QY 428 YRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKNPVNNLIRKDY 487
DB 421 YRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKNPVNNLIRKDY 480
QY 488 EEPEKTOVNNVNLNRPFRPMDYYEDLKMGKMFVSDHYDENEDDLVSHVDGSVISRREW 547
DB 481 EEPEKTOVNNVNLNRPFRPMDYYEDLKMGKMFVSDHYDENEDDLVSHVDGSVISRREW 540
QY 548 YV 549
DB 541 YV 542

RESULT 5

US-09-959-845-2
; Sequence 2, Application US/09959845
; Publication No. US2003008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroaki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-2

Query Match 94.3%; Score 2739; DB 10; Length 549;
Best Local Similarity 93.3%; Pred. No. 8.3e-202;
Matches 512; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MARTPGSPICPGGGKQAQLSSASLLGAGLLIQPTPPPLLLPFLLLFSLRCGALAGPI 60
DB 1 MARTPGSPICPGGGKQAQLSSASLLGAGLLIQPTPPPLLLPFLLLFSLRCGALAGSI 60
QY 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
DB 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPD 180
DB 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPPTFRAR 240

Db 181 LIDGNETVAACVAAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
Qy 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDQGWPGGLASDNTLHFVHPLTFNYSGVVICKVTNSLQORSODOKVIYISDPPT 360
Db 301 KSVMSRLDQGWPGGLASDNTLHFVHPLTFNYSGVVICKVTNSLQORSODOKVIYISDPPT 360
Qy 361 TTTLOPTIOQHPSTADIEDLATEPKKLPPPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTVQWSSPADVDIATEHKKLPPPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Qy 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELSDSPDSVKKENKPNVNN 480
Db 421 TTTLOPTVQWSSPADVDIATEHKKLPPPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Qy 481 LIRKDYLEBPEKTOAWNVENLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEBPEKTOAWNVENLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Qy 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 6

US-09-972-268-17
; Sequence 17, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-17

Query Match 94.3%; Score 2739; DB 10; Length 549;
Best Local Similarity 93.3%; Pred. No. 8.3e-202;
Matches 512; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MARTPGSPILCPGGKQAQLSSALLGAGLLLOPTPPPLLLLPLLLFRLCGALAGPI 60
Db 1 MARTPGSPILCPGGKQAQLSSALLGAGLLLOPTPPPLLLLPLLLFRLCGALAGSI 60
Qy 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQYQGR 120
Db 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRFAR 240
Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRFAR 240
Qy 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300

Db 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDQGWPGGLASDNTLHFVHPLTFNYSGVVICKVTNSLQORSODOKVIYISDPPT 360
Db 301 KSVMSRLDQGWPGGLASDNTLHFVHPLTFNYSGVVICKVTNSLQORSODOKVIYISDPPT 360
Qy 361 TTTLOPTIOQHPSTADIEDLATEPKKLPPPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTVQWSSPADVDIATEHKKLPPPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Qy 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELSDSPDSVKKENKPNVNN 480
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELSDSPDSVKKENKPNVNN 480
Qy 481 LIRKDYLEBPEKTOAWNVENLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEBPEKTOAWNVENLNRPERPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Qy 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 7

US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match 73.6%; Score 2138; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 9.8e-156;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTPGSPILCPGGKQAQLSSALLGAGLLLOPTPPPLLLLPLLLFRLCGALAGPI 60
Db 1 MARTPGSPILCPGGKQAQLSSALLGAGLLLOPTPPPLLLLPLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQYQGR 120
Db 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRFAR 240
Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRFAR 240
Qy 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300

Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
 Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
 Qy 361 TTTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIAT 404
 Db 361 TTTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIAT 404

RESULT 8

US-09-972-268-13
 ; Sequence 13, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanslow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,557
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 634
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
 US-09-972-268-13

Query Match 73.6%; Score 2138; DB 10; Length 634;
 Best Local Similarity 100.0%; Pred. No. 1.7e-155;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARTPGSPCLPCGGKAQLSSASLLGALLQPPPTPLLLLPPLLLFSLRCGALAGPI 60
 Db 1 MARTPGSPCLPCGGKAQLSSASLLGALLQPPPTPLLLLPPLLLFSLRCGALAGPI 60
 Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
 Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
 Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFNETATIIISQYKLPPTREAR 240
 Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFNETATIIISQYKLPPTREAR 240
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
 Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
 Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
 Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
 Qy 361 TTTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIAT 404
 Db 361 TTTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIAT 404

RESULT 9

US-09-972-268-10
 ; Sequence 10, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.

; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanslow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,557
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 510
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
 ; OTHER INFORMATION: from human Nectin-3 beta
 US-09-972-268-10

Query Match 66.2%; Score 1924.5; DB 10; Length 510;
 Best Local Similarity 67.9%; Pred. No. 3.3e-139;
 Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
 Qy 1 MARTPGSPCLPCGGKAQLSSASLLGALLQPPPTPLLLLPPLLLFSLRCGALAGPI 60
 Db 1 MARTPGSPCLPCGGKAQLSSASLLGALLQPPPTPLLLLPPLLLFSLRCGALAGPI 60
 Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
 Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
 Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFNETATIIISQYKLPPTREAR 240
 Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFNETATIIISQYKLPPTREAR 240
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
 Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
 Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
 Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPT 360
 Qy 361 TTTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVWGALFVLVS 420
 Db 361 TTTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVWGALFVLVS 420
 Qy 421 VLAFIFCYRRRTFRGDFYFARNY-IPPSDMQKESQIDVLQOQDELDSPDSYKKNQKPV- 478
 Db 421 VLAFIFCYRRRTFRGDFYFARNY-IPPSDMQKESQIDVLQOQDELDSPDSYKKNQKPV- 478
 Qy 384 IFVTVLTLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424
 Db 384 IFVTVLTLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424
 Qy 479 -NNLRKDYLEEPKTOV-----NNVENLNRFP-RRPMYVEDLKMGMKFVSD----- 523
 Db 479 -NNLRKDYLEEPKTOV-----NNVENLNRFP-RRPMYVEDLKMGMKFVSD----- 523
 Qy 425 QKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGEDIQOQMYPLYNQM 482
 Db 425 QKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGEDIQOQMYPLYNQM 482
 Qy 524 -----EYDENEDDLVSHVDSGVISRRREYV 549
 Db 524 -----EYDENEDDLVSHVDSGVISRRREYV 549
 Qy 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510
 Db 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510

RESULT 10

US-09-972-268-14
 ; Sequence 14, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.

```
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match          55.6%; Score 1907; DB 10; Length 595;
Best Local Similarity 76.4%; Pred. No. 9.2e-138;
Matches 383; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

Qy 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPPLLLFRLCGALAGPI 60
Db 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPPLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
Db 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRITCVVKHPALEKDIRSFILDIQYAPEVSVTYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRITCVVKHPALEKDIRSFILDIQYAPEVSVTYDGNWFGVGRKGVNLCNADANPPPF 300
Qy 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
Db 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
Qy 361 TTTLQ-----PTIQWHPSTADIEDLATPEPKLPPLPLSTLTIKDDTIATII 406
Db 361 KQTSRSRCDKTHTCPPCPAEAGAPSV-----FLFPFK-----PKDTLMISRPEVTCVV 411
Qy 407 ASVVGGAFLFVLSVLAGIFCYRRRTFRGDYFAKNYIPSPDMQKESQIDVLQDELDSY 466
Db 412 DVVSHEDPEVKFNWYVDGVEVHNAKTPREQYNSTY-----RVVSVLTVLHQDWLNGK 465
Qy 467 PDSVKKENK---NPVNNLRK 484
Db 466 EYCKKVSNKALPAPIEKTISK 486

RESULT 11
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
```

```
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match          65.6%; Score 1906.5; DB 10; Length 510;
Best Local Similarity 67.6%; Pred. No. 8.1e-138;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;

Qy 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPPLLLFRLCGALAGPI 60
Db 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPPLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
Db 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRITCVVKHPALEKDIRSFILDIQYAPEVSVTYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRITCVVKHPALEKDIRSFILDIQYAPEVSVTYDGNWFGVGRKGVNLCNADANPPPF 300
Qy 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
Db 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360
Qy 361 TTTLQTIQWHPSTADIEDLATPEPKLPPLPLSTLTIKDDTIATIIASVVGGAFLFVLS 420
Db 360 -----FKQTSSTAVAGAVIGAVLALFIIA 383
Qy 421 VLAGIFCYRRRTFRGDYFAKNY-IPSPDMQKESQIDVLQDELDSVPSVKENKPNV- 478
Db 384 IFVTVLLTTPKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424
Qy 479 -NNLRKDYLEEPEKTQW-----NNVENLNR-ERPMDYVEDLKMGMKFVSD----- 523
Db 425 OKDLFQPEHL--PLQTFKEREVGNLQHSNLSRFDYEDENPVGSDGIQQMYPLYNQM 482
Qy 524 -----EYHDENEDDLVSHVDGVSISRREWTV 549
Db 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510

RESULT 12
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
```

```

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match      65.3%; Score 1896; DB 10; Length 387;
Best Local Similarity 98.9%; Pred. No. 3.5e-137;
Matches 359; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPI 60
DB 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPI 60

QY 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQYQGR 120
DB 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQYQGR 120

QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPD 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPD 180

QY 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTTFFNETATIIISQYKLFPTFRFAR 240
DB 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTTFFNETATIIISQYKLFPTFRFAR 240

QY 241 GRRITCVVHPALEKDIYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPP 300
DB 241 GRRITCVVHPALEKDIYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPP 300

QY 301 KSVWSRLDQWPDGLASDNLTHFVHPLTFNYSGVYICKVNTSLGORSQDKVIYISDPPT 360
DB 301 KSVWSRLDQWPDGLASDNLTHFVHPLTFNYSGVYICKVNTSLGORSQDKVIYISDPPT 360

QY 361 TTT 363
DB 361 KQT 363

RESULT 13
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match      65.1%; Score 1892.5; DB 10; Length 504;
Best Local Similarity 67.6%; Pred. No. 9.5e-137;
Matches 384; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

QY 7 PSLPCGGKAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPIVPHV 66

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DB 1 PSLPCGGKAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPIVPHV 60
QY 67 TAVGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQYQGRVLPKNY 126
DB 61 TAVGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQYQGRVLPKNY 120
QY 127 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPD 186
DB 121 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPD 180
QY 187 ETVAACIAATGKPAHIDWEGDLGEMESTTTTFFNETATIIISQYKLFPTFRFAR 246
DB 181 ETVAACIAATGKPAHIDWEGDLGEMESTTTTFFNETATIIISQYKLFPTFRFAR 240
QY 247 VVKHPALEKDIYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPPKSVWSR 306
DB 241 VVKHPALEKDIYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPPKSVWSR 300
QY 307 LDGQWPDGLASDNLTHFVHPLTFNYSGVYICKVNTSLGORSQDKVIYISDPPT 366
DB 301 LDGQWPDGLASDNLTHFVHPLTFNYSGVYICKVNTSLGORSQDKVIYISDPPT 360
QY 367 TIQWHPSTADIEDLATEPKLPPLSTLATIKDITATIIASVVGGALFVLVSLAGIF 426
DB 364 -----FKQTSSTAVAGAVIGAVLALFIATFVL 383
QY 427 CYRRRTFRGDIYFKNY-IPSPDMQKESQIDVLQDDELSDYPSVKENKNPV--NNLIR 483
DB 384 LTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLPQKDLFQ 424
QY 484 KDYLEEPEKTQW-----NNVENLRF--ERPMDYVEDLKMGMKFVSD----- 523
DB 425 PEHL--PLQTFKEREVGNLOHNSGLNRSFDEDEPNVGEDGIQQMYPLYNOMCYODRS 482
QY 524 --EHDYENEDDLVSHVDGVSISREWYV 549
DB 483 PGKHQNDPKRV-----YIDPREHV 504

RESULT 14
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match      65.0%; Score 1888.5; DB 10; Length 437;
Best Local Similarity 78.9%; Pred. No. 1.6e-136;
Matches 370; Conservative 16; Mismatches 34; Indels 49; Gaps 4;

QY 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPI 60
DB 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRCLGALAGPI 60
QY 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQYQGR 120

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Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGR 120
Qy 121 VLFKNYSINDATITLHNIGFSDSKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGNLKCNDADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGNLKCNDADANPPPF 300
Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTSNLSGORSQOKVYIISDPPT 360
Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTSNLSGORSQOKVYIISDPV- 359
Qy 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420
Db 360 -----FKQTSSIAVAGAVIGAVLALFIIA 383
Qy 421 VLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES-----QIDVLQ 459
Db 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430

RESULT 15
US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoehimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4
```

```
Query Match 63.1%; Score 1832.5; DB 10; Length 510;
Best Local Similarity 66.8%; Pred. No. 4e-132;
Matches 376; Conservative 39; Mismatches 81; Indels 67; Gaps 10;

Qy 1 MARTPGSPPLCPGGKQAQLSSASLLGALLQPTTPLLPLLLFSLRCLGALAGPI 60
Db 1 MARTPGAPLCPGGKQAQLSAFPAPAGLLLPATPPPLLLPLLLFSLRCLGALAGSI 60

Qy 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGR 120
Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDYQGR 120

Qy 121 VLFKNYSINDATITLHNIGFSDSKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACVAAATGKPAQIDWEGDLGEMESTTSPNETATIVSQYKLPFTRFAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGNLKCNDADANPPPF 300
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Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGNLKCNDADANPPPF 300
Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTSNLSGORSQOKVYIISDPPT 360
Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTSNLSGORSQOKVYIISDPL 360
Qy 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVS 420
Db 361 TQT-----SSIA-----VAGAVIGAVLALFIIT 383
Qy 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK-----ESQIDVLOQDEL-----DSYPSVSK 472
Db 384 VFTVLLTPRKK--RPSYLDKVIDLPPTHKPPVYEEIRPSLPQKDLGQTEHLPLQTQF 441
Qy 473 ENK-----NPVNNLIRKDYLERPEKT-OWNNVENLNRFERPMDYIEDLKXGKMFVDEHY 526
Db 442 KEGAGGLQFSNGPISRRFDYEDSTMQEDGTQMCPLYSQMCHQDRSPR-----QHH 494
Qy 527 DENEDDLVSHVDGSGVISRREWYV 549
Db 495 PRNPERL-----YINPREHYV 510
```

Search completed: October 6, 2005, 09:33:41
Job time : 257.269 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 90.6763 Seconds
(without alignments)
2341.642 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 2901

Sequence: 1 MARI LRSP LCPGGGKAQLS.....EDDLVSHVDGVSISRREYV 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_l6Dec04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2901 | 100.0 | 549 | 5 | Aae23283 Human nec |
| 2 | 2901 | 100.0 | 549 | 6 | Abj20222 Human IG |
| 3 | 2901 | 100.0 | 549 | 8 | Adr66369 Human pro |
| 4 | 2901 | 100.0 | 549 | 8 | Adr66711 Human pro |
| 5 | 2887 | 99.5 | 549 | 5 | Aae23282 Mouse nec |
| 6 | 2866 | 98.8 | 542 | 5 | Aae23281 Human del |
| 7 | 2856 | 98.4 | 555 | 4 | Aam39143 Human pol |
| 8 | 2721 | 93.8 | 549 | 4 | Aag63982 Amino aci |
| 9 | 2721 | 93.8 | 549 | 4 | Aag63985 Amino aci |
| 10 | 2721 | 93.8 | 549 | 5 | Aae23291 Mouse nec |
| 11 | 2568 | 88.5 | 559 | 4 | Aam40929 Human pol |
| 12 | 2120 | 73.1 | 426 | 5 | Aae23289 Human nec |
| 13 | 2120 | 73.1 | 634 | 5 | Aae23287 Human nec |
| 14 | 1920 | 66.2 | 510 | 5 | Aae23286 Human nec |
| 15 | 1906 | 65.7 | 510 | 5 | Aae23285 Mouse nec |
| 16 | 1902 | 65.6 | 437 | 5 | Aae23299 Human nec |
| 17 | 1892 | 65.2 | 504 | 5 | Aae23284 Human del |
| 18 | 1889 | 65.1 | 595 | 5 | Aae23288 Human nec |
| 19 | 1878 | 64.7 | 387 | 5 | Aae23290 Human nec |
| 20 | 1814 | 62.5 | 510 | 4 | Aag63983 Amino aci |
| 21 | 1814 | 62.5 | 510 | 5 | Aae23292 Mouse nec |
| 22 | 1809 | 62.4 | 438 | 4 | Aag63984 Amino aci |
| 23 | 1809 | 62.4 | 438 | 5 | Aae23293 Mouse nec |
| 24 | 1621 | 55.9 | 305 | 5 | Adr41425 Human CD- |
| 25 | 1355 | 46.7 | 258 | 5 | Abb90250 Human pol |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 1235 | 42.6 | 267 | 4 | AAM93536 Human pol |
| 27 | 1235 | 42.6 | 267 | 8 | ADL31248 Human pro |
| 28 | 649.5 | 22.4 | 514 | 6 | ABJ20237 Human IG |
| 29 | 649.5 | 22.4 | 517 | 3 | RAY32390 Herpesvir |
| 30 | 649.5 | 22.4 | 517 | 5 | AAE23294 Human nec |
| 31 | 627 | 21.6 | 518 | 5 | ABG77170 Prostate |
| 32 | 569 | 19.6 | 458 | 5 | AAE23295 Human nec |
| 33 | 555 | 19.1 | 581 | 8 | ADP03590 Infection |
| 34 | 551 | 19.0 | 580 | 8 | ADO47877 Alpha-Her |
| 35 | 548 | 18.9 | 510 | 8 | ADK83174 Human 191 |
| 36 | 548 | 18.9 | 510 | 8 | ADK83200 Human 191 |
| 37 | 544 | 18.8 | 510 | 4 | AAU00471 Human TAN |
| 38 | 544 | 18.8 | 510 | 5 | ABJ05562 Breast ca |
| 39 | 544 | 18.8 | 510 | 6 | ABR48229 Human bla |
| 40 | 544 | 18.8 | 510 | 6 | ABU56613 Lung canc |
| 41 | 544 | 18.8 | 510 | 6 | ABP97212 Tumour-as |
| 42 | 544 | 18.8 | 510 | 7 | ADB80512 Ovarian c |
| 43 | 544 | 18.8 | 510 | 7 | ADM42033 Human TAN |
| 44 | 544 | 18.8 | 510 | 7 | ADN38748 Cancer/an |
| 45 | 544 | 18.8 | 510 | 8 | ADK83210 Human IG |

ALIGNMENTS

RESULT 1
AAE23283

ID AAE23283 standard; protein; 549 AA.

XX AC AAE23283;

XX AC AAE23283;

DT 27-AUG-2002 (first entry)

XX DE Human nectin-3alpha protein.

XX KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;

XX KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

XX KW allograft rejection; metastasis; resenosis; inflammatory bowel disease;

XX KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

XX KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 73

FT Domain /note= "N-glycosylated"

FT Domain /note= "Extracellular Ig domain"

FT Modified-site 83

FT Modified-site 125

FT Modified-site /note= "N-glycosylated"

FT Modified-site 186

FT Domain /note= "N-glycosylated"

FT Domain /note= "N-glycosylated"

FT Modified-site 222

FT Domain /note= "N-glycosylated"

FT Domain /note= "Extracellular Ig domain"

FT Modified-site 331

FT Modified-site /note= "N-glycosylated"

FT Domain /note= "Transmembrane domain"

FT Domain /note= "C-terminal domain"

XX WO200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

Db 1 MARTLRSPCLPGGKAQLSSASLLGAGLLLOPTPPPLLLLPFLLSRLCGALAGPI 60
 Qy 61 IVEPHVTAVGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYGR 120
 Db 61 IVEPHVTAVGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYGR 120
 Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240
 Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240
 Qy 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWVFGKGNLKNADANPPPF 300
 Db 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWVFGKGNLKNADANPPPF 300
 Qy 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGORSOKVYIISDPPT 360
 Db 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGORSOKVYIISDPPT 360
 Qy 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFVLVS 420
 Db 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFVLVS 420
 Qy 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMOKESQIDVLQDELDSDYPSVKKNKPNVN 480
 Db 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMOKESQIDVLQDELDSDYPSVKKNKPNVN 480
 Qy 481 LIRKDYLEPEKQWNNVENLNRPERMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
 Db 481 LIRKDYLEPEKQWNNVENLNRPERMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
 Qy 541 VISRREWYV 549
 Db 541 VISRREWYV 549

RESULT 3

ID ADR66369 standard; protein; 549 AA.

XX ADR66369;

AC ADR66369;

DT 02-DEC-2004 (first entry)

DE Human prostatic carcinoma derived protein SEQ ID 223 #2.

XX human; cytostatic; diagnosis; prostatic cancer;

KW differential expression analysis.

XX Homo sapiens.

XX W0204076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

PR 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.

PA (PILA/) PILARSKY C.

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;

PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;

PI Xinzhong L, Staub E;

XX WPI; 2004-653386/63.
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding agents.
 PT Claim 2; Page 703; 1607pp; German.
 XX This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

XX SQ Sequence 549 AA;

Query Match 100.0%; Score 2901; DB 8; Length 549;

Best Local Similarity 100.0%; Pred. No. 2.1e-233;

Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTLRSPCLPGGKAQLSSASLLGAGLLLOPTPPPLLLLPFLLSRLCGALAGPI 60

Db 1 MARTLRSPCLPGGKAQLSSASLLGAGLLLOPTPPPLLLLPFLLSRLCGALAGPI 60

Qy 61 IVEPHVTAVGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYGR 120

Db 61 IVEPHVTAVGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180

Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240

Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFAR 240

Qy 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWVFGKGNLKNADANPPPF 300

Db 241 GRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWVFGKGNLKNADANPPPF 300

Qy 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGORSOKVYIISDPPT 360

Db 301 KSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGORSOKVYIISDPPT 360

Qy 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFVLVS 420

Db 361 TTTLQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFVLVS 420

| | | | | | |
|----------|---|--|-----|----------|---|
| QY | 421 | VLGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKENKPNVNN | 480 | CC | between normal and tumorous tissues, with (over)expression being detected |
| Db | 421 | VLGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKENKPNVNN | 480 | CC | by quantitative PCR. Analysis of prostatic cancer samples showed that |
| QY | 481 | LIRKDYLEPEKQWNNVENLNRFRPMDYYEDLKMGKFPVSDHYDENEDDLVSHVDGS | 540 | CC | CD24 was upregulated in many of them. Sections of tissue, isolated from |
| Db | 481 | LIRKDYLEPEKQWNNVENLNRFRPMDYYEDLKMGKFPVSDHYDENEDDLVSHVDGS | 540 | CC | prostatic cancer patients, or subjects at risk, were incubated |
| QY | 541 | VISRREWYV 549 | | CC | sequentially with anti-human CD4 murine monoclonal antibodies; |
| Db | 541 | VISRREWYV 549 | | CC | biotinylated second antibody; streptavidin-conjugated horseradish |
| RESULT 4 | | | | CC | peroxidase and then diaminobenzidine as colour former (brown). The |
| ADRe6711 | | | | CC | samples were counterstained with hemalum (blue). Malignant cells stained |
| ID | ADR66711 | standard; protein; 549 AA. | | CC | strongly but non-malignant cells only weakly. In 15 of 63 samples of |
| AC | ADR66711; | | | CC | adenocarcinoma, membrane and cytoplasmic staining was very strong, and |
| DT | 02-DEC-2004 | (first entry) | | CC | lymph node metastases were also stained. ADR66711 represent the |
| DE | Human prostatic carcinoma derived protein SEQ ID 223 #3. | | | CC | polynucleotide and polypeptide sequences used in the method of the |
| XX | human; cytostatic; diagnosis; prostatic cancer; | | | XX | invention. |
| KW | differential expression analysis. | | | XX | Sequence 549 AA; |
| XX | Homo sapiens. | | | QY | Query Match 100.0%; Score 2901; DB 8; Length 549; |
| OS | | | | Db | Best Local Similarity 100.0%; Pred. No. 2.1e-233; |
| PN | WO2004076614-A2. | | | QY | Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| XX | 10-SEP-2004. | | | Db | 1 MARTLPSPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLLSRLCGALAGPI 60 |
| XX | 22-FEB-2004; 2004WO-DE000433. | | | QY | 1 MARTLPSPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLLSRLCGALAGPI 60 |
| PR | 17-FEB-2003; 2003DE-01009985. | | | QY | 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQVGFSGYQGR 120 |
| PR | 14-MAY-2003; 2003DE-01022134. | | | Db | 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQVGFSGYQGR 120 |
| XX | (HINZ/) HINZMANN B. | | | QY | 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180 |
| PA | (DAHL/) DAHL E. | | | Db | 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180 |
| PA | (ROSE/) ROSENTHAL A. | | | QY | 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFR 240 |
| PA | (HERM/) HERMANN K. | | | Db | 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFR 240 |
| PA | (PILA/) PILARSKY C. | | | QY | 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300 |
| XX | Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T; | | | Db | 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300 |
| PI | Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S; | | | QY | 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDOKVIYISDPPT 360 |
| PI | Xinzhong L, Staub E; | | | Db | 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDOKVIYISDPPT 360 |
| XX | WPI; 2004-653386/63. | | | QY | 361 TTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDITATIIASVVGALFVLVS 420 |
| XX | New nucleic acids, and encoded proteins, from prostatic cancer tissue, | | | Db | 361 TTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDITATIIASVVGALFVLVS 420 |
| PT | useful for diagnosis, treatment and in screening for specific binding | | | QY | 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKENKPNVNN 480 |
| PS | agents. | | | Db | 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKENKPNVNN 480 |
| PS | Claim 2; Page 1205; 1607pp; German. | | | QY | 481 LIRKDYLEPEKQWNNVENLNRFRPMDYYEDLKMGKFPVSDHYDENEDDLVSHVDGS 540 |
| XX | This invention describes novel cytostatic polynucleotide and polypeptide | | | Db | 481 LIRKDYLEPEKQWNNVENLNRFRPMDYYEDLKMGKFPVSDHYDENEDDLVSHVDGS 540 |
| CC | sequences which can be used in a method for diagnosing prostatic cancer | | | QY | 541 VISRREWYV 549 |
| CC | or the risk of developing prostatic cancer. Diagnosis is based on | | | Db | 541 VISRREWYV 549 |
| CC | determining over transcription or over expression of the sequences in | | | RESULT 5 | |
| CC | prostatic tissue. Screening for inhibitors of the sequences or detection | | | AAE23282 | standard; protein; 549 AA. |
| CC | substances involves a binding assay, any compounds that bind are | | | ID | AAE23282 |
| CC | selected, optionally after deconvolution of mixtures. Detection of a | | | XX | AAE23282; |
| CC | predetermined minimum level of the reporter indicates the presence of | | | XX | AC |
| CC | tumour cells. Inhibitors can be chosen from antisense oligonucleotides, | | | XX | DT |
| CC | short-interfering RNA or ribozymes; an organic molecule of molecular | | | XX | 29-AUG-2003 (revised) |
| CC | weight below 5000, preferably 300, that binds to the polypeptide; an | | | DT | 27-AUG-2002 (first entry) |
| CC | aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the | | | XX | Mouse nectin-3-human nectin 3alpha fusion protein. |
| CC | polypeptide, preferably humanised or human; an anti-idiotypic, non-human | | | XX | Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis; |
| CC | (monoclonal) antibody directed against Ab or any of the above derivatised | | | XX | |
| CC | with a reporter group, cell toxin, immunostimulatory molecules and/or | | | XX | |
| CC | radioisotope. The polynucleotides are identified in human prostatic | | | XX | |
| CC | cancer by differential expression analysis, using DNA microarrays, | | | XX | |

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
 KW stroke; cancer; herpesvirus infection; asthma; fusion protein;
 KW chromosome 3.

XX Homo sapiens.
 OS Mus musculus.
 OS Chimeric.

XX Key Location/Qualifiers
 FT Region 1..7
 FT /note= "Mouse nectin-3 protein"
 FT Region 8..549
 FT /note= "Human nectin-3alpha protein"

XX W0200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX N-PSDB; AAD37441.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.

XX Claim 1; Page 80-82; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein containing
 CC mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
 CC alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX Sequence 549 AA;

Query Match 99.5%; Score 2887; DB 5; Length 549;
 Best Local Similarity 99.6%; Pred. No. 3.1e-232;
 Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARTLRSPICPGGGKQAQLSSALLGALLLQPTPPPPPLLLLPPLLLFRLCGALAGPI 60

DB 1 MARTPGSPICPGGGKQAQLSSALLGALLLQPTPPPPPLLLLPPLLLFRLCGALAGPI 60

QY 61 IVEPHVTAVMGKNVSLKCLLEVNETTIQISWEKHGKSSQTVAVHPQYGFSGVQYQGR 120

DB 61 IVEPHVTAVMGKNVSLKCLLEVNETTIQISWEKHGKSSQTVAVHPQYGFSGVQYQGR 120

QY 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATITISQYKLPPTPFAR 240
 DB 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATITISQYKLPPTPFAR 240
 QY 241 GRRITCVVKKHPPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
 DB 241 GRRITCVVKKHPPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
 QY 301 KSVMSRLDGGWPDGLLASDNTLHFVHPLTNYSGVYCKVTNSLGQRSDQKVIYISDPPT 360
 DB 301 KSVMSRLDGGWPDGLLASDNTLHFVHPLTNYSGVYCKVTNSLGQRSDQKVIYISDPPT 360
 QY 361 TTTLQPTIOHHPSTADIEDLATEPKLPFPFLSTLATIKDDTIATIIASVVGALFVILVS 420
 DB 361 TTTLQPTIOHHPSTADIEDLATEPKLPFPFLSTLATIKDDTIATIIASVVGALFVILVS 420
 QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPVNN 480
 DB 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPVNN 480
 QY 481 LIRKDYLEEPKTOANNVNNLNRPERPMDYEDLKMGKFFVSDHYDENEDDLVSHVDGS 540
 DB 481 LIRKDYLEEPKTOANNVNNLNRPERPMDYEDLKMGKFFVSDHYDENEDDLVSHVDGS 540
 QY 541 VISRREWYV 549
 DB 541 VISRREWYV 549

RESULT 6

AAE23281 ID AAE23281 standard; protein; 542 AA.

XX AC AAE23281;

XX 27-AUG-2002 (first entry)

XX Human deleted nectin-3alpha protein.

XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.

XX Homo sapiens.

XX W0200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX N-PSDB; AAD37440.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.

XX Claim 1; Page 76-78; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha protein
CC containing 7 amino acids deleted from the N-terminal end. Human nectin-
CC 3alpha gene is located on chromosome 3
XX
SQ Sequence 542 AA;

Query Match 98.8%; Score 2866; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.7e-230; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0;

QY 8 SPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLFSLRLCGALAGPIIIVPHVT 67
DB 1 SPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLFSLRLCGALAGPIIIVPHVT 60
QY 68 AVGNKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGRVLFKNYS 127
DB 61 AVGNKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGRVLFKNYS 120
QY 128 LNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSGTTVTVLVEPTVSLIKGPDLSLDGNE 187
DB 121 LNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSGTTVTVLVEPTVSLIKGPDLSLDGNE 180
QY 188 TAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISOYKLPPTPFARGRRITCV 247
DB 181 TAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISOYKLPPTPFARGRRITCV 240
QY 248 VKHPALEKDIRYFILDIOVAPEVSVTGYDGNMFGKGNLKNADANPPPKFSVMSRL 307
DB 241 VKHPALEKDIRYFILDIOVAPEVSVTGYDGNMFGKGNLKNADANPPPKFSVMSRL 300
QY 308 DGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVYISDPTTTTLQPT 367
DB 301 DGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVYISDPTTTTLQPT 360
QY 368 IQWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGGLFVLVSVLAGIFC 427
DB 361 IQWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGGLFVLVSVLAGIFC 420
QY 428 YRRRTFRGDFYAKNYIPPSDMQKESQIDVLQDELSDYSPSVKKNPNVNLIRKDYL 487
DB 421 YRRRTFRGDFYAKNYIPPSDMQKESQIDVLQDELSDYSPSVKKNPNVNLIRKDYL 480
QY 488 EEPKTOQNNVENLNRRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISREW 547
DB 481 EEPKTOQNNVENLNRRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISREW 540
QY 548 YV 549
DB 541 YV 542

RESULT 7
AAM39143
ID AAM39143 standard; protein; 555 AA.
XX

AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
FN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58239.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2288; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 555 AA;

Query Match 98.4%; Score 2856; DB 4; Length 555;
Best Local Similarity 99.8%; Pred. No. 1.2e-229;
Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLFSLRLCGALAGPIIIVPHVTA 68
DB 15 PLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLFSLRLCGALAGPIIIVPHVTA 74
QY 69 VWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGRVLFKNYS 128
XX

Db 75 VWGNVSLKCLIEVNETITQISWEKIHCKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYSL 134
 Qy 129 NDATITLHNIGFSDSGYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNET 188
 Db 135 NDATITLHNIGFSDSGYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNET 194
 Qy 189 VAAICIAATGKPAHIDWEGDLGEMESTTTTSPNETATITISQYKLPPTFARGRRITCVV 248
 Db 195 VAAICIAATGKPAHIDWEGDLGEMESTTTTSPNETATITISQYKLPPTFARGRRITCVV 254
 Qy 249 KHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNVLCNADANPPFPFKSVWSRLD 308
 Db 255 KHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNVLCNADANPPFPFKSVWSRLD 314
 Qy 309 GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPPTTLOPTI 368
 Db 315 GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPPTTLOPTI 374
 Qy 369 QWHPSTADIEDLATEPKKLPPLSTLATIKDDTITATIIASVVGALFVLVSVLAGIFCY 428
 Db 375 QWHPSTADIEDLATEPKKLPPLSTLATIKDDTITATIIASVVGALFVLVSVLAGIFCY 434
 Qy 429 RRRRTFRGDYFAKNYIPPSDMOKESQIDVLQODELDSYPSDKKNPNVNNLIRKDYLE 488
 Db 435 RRRRTFRGDYFAKNYIPPSDMOKESQIDVLQODELDSYPSDKKNPNVNNLIRKDYLE 494
 Qy 489 EPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISRREWY 548
 Db 495 EPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISRREWY 554
 Qy 549 V 549
 Db 555 V 555

RESULT 8

AAG63982
 ID AAG63982 standard; protein; 549 AA.

XX AC AAG63982;

XX 26-NOV-2001 (first entry)

DT Amino acid sequence of murine nectin-3.

DE Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

KW Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX 09-MAR-2000; 2000JP-00065595.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA (TAKA/) TAKAHASHI K.

XX Takahashi K, Takai Y, Nakanishi H, Sato K;

XX WPI; 2001-570771/64.

XX N-PSDB; AAH78179.

XX New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and corresponding antibodies.

XX Claim 1; Page 37-40; 64pp; Japanese.

XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic

CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer

XX SQ Sequence 549 AA;

Query Match 93.8%; Score 2721; DB 4; Length 549;
 Best Local Similarity 92.9%; Pred. No. 2.4e-218;
 Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MARIPLRSPPLCPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFRLCGALAGPI 60

Db 1 MARIPLRSPPLCPGGKQAQLSSAFPPAAGLLLPAPTPPPLLLLPPLLLFRLCGALAGSI 60

Qy 61 IVPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGR 120

Db 61 IVPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHHPQYGFVSQGEYQGR 120

Qy 121 VLPKNYSLNDATITLHNIGFSDSGYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPD 180

Db 121 VLPKNYSLNDATITLHNIGFSDSGYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSPNETATITISQYKLPPTFAR 240

Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSPNETATITISQYKLPPTFAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNVLCNADANPPFP 300

Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNVLCNADANPPFP 300

Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360

Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDPPT 360

Qy 361 TTTLQPTVQWSSPADYQDTEHKKLPPLSTLATIKDDTITATIIASVVGALFVLV 420

Db 361 TTTLQPTVQWSSPADYQDTEHKKLPPLSTLATIKDDTITATIIASVVGALFVLV 420

Qy 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMOKESQIDVLQODELDSYPSDKKNPNVNN 480

Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMOKESQIDVLQODELDSYPSDKKNPNVNN 480

Qy 481 LIRKDYLEEEPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540

Db 481 LIRKDYLEEEPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540

Qy 541 VISRREWYV 549

Db 541 VISRREWYV 549

RESULT 9

AAG63985

ID AAG63985 standard; protein; 549 AA.

XX AC AAG63985;

XX 26-NOV-2001 (first entry)

DT Amino acid sequence of murine nectin-3.

DE Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

KW Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX

PR 09-MAR-2000; 2000JP-00065595.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA (TAKA/) TAKAHASHI K.
 XX Takahashi K, Takai Y, Nakanishi H, Sato K;
 PI WPI; 2001-570771/64.
 XX N-PSDB; AAH78182.
 DR New protein family for diagnosing and treating tumor infiltration and
 XX metastasis comprises the mouse nectin-3 protein families and
 PT corresponding antibodies.
 PT
 XX
 PS Disclosure; Page 56-61; 64pp; Japanese.
 XX
 CC The present sequence represents a murine nectin-3 polypeptide. Nectin-3
 CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
 CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
 CC polynucleotides are useful for investigating the mechanisms of cell
 CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
 CC malignancies of various cancers, and the development of methods for the
 CC treatment and prevention of cancer
 XX
 SQ Sequence 549 AA;

Query Match 93.8%; Score 2721; DB 4; Length 549;
 Best Local Similarity 92.9%; Pred. No. 2.4e-218;
 Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 MARTLRSPICPGGKAQLSSASILGAGLLQLQPTPPPLLLLPFLLSRLCGALAGPI 60
 DB 1 MARTPGAPICPGGKAQLSSAPPAAGLLLPAPTPLLLLPFLLSRLCGALAGSI 60
 QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSTQTVAVHHPQYGSVQYQGR 120
 DB 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSTQTVAVHHPQYGSVQYQGR 120
 QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAICIAATGKPAHIDWEGDLGEMSTTSPNETATIIISQYKLPFTRFAR 240
 DB 181 LIDGNETVAICIAATGKPAHIDWEGDLGEMSTTSPNETATIIISQYKLPFTRFAR 240
 QY 241 GRITCVVHPALEKDIRYFILDIOYAPEVSVTVGDNWFGVGRKGNLKNADANPPF 300
 DB 241 GRITCVVHPALEKDIRYFILDIOYAPEVSVTVGDNWFGVGRKGNLKNADANPPF 300
 QY 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTENYSGVYICKVTNSIGORSOKVYISDPPT 360
 DB 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTENYSGVYICKVTNSIGORSOKVYISDPPT 360
 QY 361 TTTLQPTQIOWHPSTADIEATEPKLPFPLSTLATIKDDTIATIIASVVGALFVLVS 420
 DB 361 TTTLQPTQIOWHPSTADIEATEPKLPFPLSTLATIKDDTIATIIASVVGALFVLVS 420
 QY 421 VLAGIFCYRRRTFRGYFPAKNYIPPSDMQKESQIDVLQDELSDYSPDKVKNKNPNVN 480
 DB 421 VLAGIFCYRRRTFRGYFPAKNYIPPSDMQKESQIDVLQDELSDYSPDKVKNKNPNVN 480
 QY 481 LIRKDYLEBEKTOVNNVNLNRRERPMYEDILKMGKFFVSDHYDENEDDLVSHVDGS 540
 DB 481 LIRKDYLEBEKTOVNNVNLNRRERPMYEDILKMGKFFVSDHYDENEDDLVSHVDGS 540
 QY 541 VISREWYV 549
 DB 541 VISREWYV 549

RESULT 10
 AAE23291

ID AAE23291 standard; protein; 549 AA.
 XX AAE23291;
 AC 27-AUG-2002 (first entry)
 DT Mouse nectin-3alpha protein.
 DE Mouse; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
 XX paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma.
 XX
 OS Mus musculus.
 XX
 PN WO200228902-A2.
 XX 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US031392.
 PF 05-OCT-2000; 2000US-0238557P.
 PR (IMMV) IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 XX WPI; 2002-426103/45.
 XX
 PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX
 PS Disclosure; Page 107-109; 141pp; English.
 XX
 CC The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is mouse nectin-3alpha protein
 XX
 SQ Sequence 549 AA;
 Query Match 93.8%; Score 2721; DB 5; Length 549;
 Best Local Similarity 92.9%; Pred. No. 2.4e-218;
 Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MARTLRSPICPGGKAQLSSASILGAGLLQLQPTPPPLLLLPFLLSRLCGALAGPI 60
 DB 1 MARTPGAPICPGGKAQLSSAPPAAGLLLPAPTPLLLLPFLLSRLCGALAGSI 60
 QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSTQTVAVHHPQYGSVQYQGR 120
 DB 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSTQTVAVHHPQYGSVQYQGR 120
 QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTVTLVEPTVSLIKGPD 180

QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTREAR 240
Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTREAR 240
QY 241 GRRITCVVGHKPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVGHKPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIVISDPPT 360
Db 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIVISDPPT 360
QY 361 TTTLOPTQWHPSPADIEDLATEKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTQWHPSPADIEDLATEKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPNVN 480
Db 421 ILAGVFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPNVN 480
QY 481 LIRKDYLEPEKTOQNNVNLNRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVNLNRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549
RESULT 11
AA40929
ID AA40929 standard; protein; 559 AA.
XX
AC AA40929;
XX
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 5860.
XX
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Sny-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN W0200153312-Al.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AA160085.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5860; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AM38642-AM42213) with nontropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Sny-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 559 AA;
Query Match 88.5%; Score 2568.5; DB 4; Length 559;
Best Local Similarity 91.3%; Pred. No. 1.4e-205;
Matches 504; Conservative 4; Mismatches 33; Indels 11; Gaps 8;
QY 9 PLCPGGGKAQLSSASLLGALLQPPPTPPPLLLLLFLLLSRLCGALAGPIIVEPHVTA 68
Db 8 PLCPGGGKAQLSSASLLGALLQPPPTPPPLLLLLFLLLSRLCGALAGPIIVEPHVTA 67
QY 69 VWGKNVSLKCLIEVNETITQISWEKHGKSQTVAHHPOYGFVSQGEYGRVLFKNYSL 128
Db 68 VWGKNVSLKCLIEVNETITQISWEKHGKSQTVAHHPOYGFVSQGEYGRVLFKNYSL 127
QY 129 NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLDGGNET 188
Db 128 NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLDGGNET 187
QY 189 VAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTREARRIITCVV 248
Db 188 VAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTREARRIITCVV 247
QY 249 KHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVWSRLD 308
Db 248 KHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVWSRLD 307
QY 309 GQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIVISDPPTTTIQLP- 366
Db 308 GQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSPGSKVETQKVHPTFQDPSLPTYPPL 367
QY 367 ---TIOW-HPSTADI-EDLATEPKKL-PPPLSTLTIKDDT-TATIIASVVG-CALFIVL 418
Db 368 PALQFQWASESTAXTSRDLATEPKKAPSPSLTILATIKGWTQPTIIIXKSGVALFIVL 427
QY 419 VSVLA-GIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNP 477
Db 428 VKCFGLGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNP 487
QY 478 VNNLIRKDYLEPEKTOQNNVNLNRPMDYYEDLKMGMKFVSDHYDENEDDLVSHV 537
Db 488 VNNLIRKDYLEPEKTOQNNVNLNRPMDYYEDLKMGMKFVSDHYDENEDDLVSHV 547
QY 538 DGSVISRREWYV 549
Db 548 DGSVISRREWYV 559
RESULT 12
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX

CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein containing
 CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
 XX
 XX Sequence 634 AA;

Query Match 73.1%; Score 2120; DB 5; Length 634;
 Best Local Similarity 99.5%; Pred. No. 5.3e-168;
 Matches 402; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTLRSPCLPGGGKAQLSSASLLGAGLLLPPTPPPLLLPFLLSRLCGALAGPI 60
 Db 1 MARTPGSPCLPGGGKAQLSSASLLGAGLLLPPTPPPLLLPFLLSRLCGALAGPI 60
 Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVOGEYQGR 120
 Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVOGEYQGR 120
 Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTEPLGNAQSSTTVTVLVEPTVSLIKGPD 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTEPLGNAQSSTTVTVLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFNETATIIISQYKLPFTRPAR 240
 Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFNETATIIISQYKLPFTRPAR 240
 Qy 241 GRRITCVVKHPALBKDIRYSFILDIQYAPESVTVGYDGNWFGKGVNKLKNADANPPPF 300
 Db 241 GRRITCVVKHPALBKDIRYSFILDIQYAPESVTVGYDGNWFGKGVNKLKNADANPPPF 300
 Qy 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIISDPPT 360
 Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIISDPPT 360
 Qy 361 TTTTLQPTIQWHPSTADIEDLATEPKLPFLPLSTLTIKDDTIAT 404
 Db 361 TTTTLQPTIQWHPSTADIEDLATEPKLPFLPLSTLTIKDDTIAT 404

RESULT 14
 AA23286
 ID AA23286 standard; protein; 510 AA.

AC AA23286;

XX 27-AUG-2002 (first entry)

XX Human nectin-3beta protein.

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 73 /note= "N-glycosylated"

FT Domain 74..152

FT Modified-site /note= "Extracellular Ig domain"
 FT 83 /note= "N-glycosylated"
 FT Modified-site 125 /note= "N-glycosylated"
 FT Modified-site 186 /note= "N-glycosylated"
 FT Domain 189..250 /note= "N-glycosylated"
 FT Modified-site 222 /note= "Extracellular Ig domain"
 FT Domain 287..342 /note= "N-glycosylated"
 FT Modified-site 331 /note= "Extracellular Ig domain"
 FT Domain 386..510 /note= "N-glycosylated"
 FT /note= "Intracellular C-terminal domain"
 XX
 XX WO200228902-A2.
 PD 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US0311392.
 XX 05-OCT-2000; 2000US-0238557P.
 XX (IMMV) IMMUNEX CORP.
 XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 PI WPI; 2002-426103/45.
 DR N-PSDB; AAD37445.
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX Claim 1; Page 98-99; 141pp; English.
 PS The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is human nectin-3beta protein.
 CC Human nectin-3beta gene is located on chromosome 3
 XX
 XX Sequence 510 AA;

Query Match 66.2%; Score 1920.5; DB 5; Length 510;
 Best Local Similarity 67.9%; Pred. No. 1.8e-151;
 Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

Qy 1 MARTLRSPCLPGGGKAQLSSASLLGAGLLLPPTPPPLLLPFLLSRLCGALAGPI 60
 Db 1 MARTLRSPCLPGGGKAQLSSASLLGAGLLLPPTPPPLLLPFLLSRLCGALAGPI 60
 Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVOGEYQGR 120
 Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGSVOGEYQGR 120

Qy 524 -----EHYDENEDDLVSHVDCSVISRREWYV 549
Db 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510

Search completed: October 6, 2005, 09:51:32
Job time : 92.6763 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: October 6, 2005, 09:42:42 ; Search time 18.0493 Seconds
(without alignments)
2926.593 Million cell updates/sec

Title: US-09-972-268-6
Perfect score: 2901
Sequence: 1 MARTLRSPCLCGGKAQLS.....EDDLVSHVDGVSISRREYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | ID | Description |
|------------|-------------|-------|--------|----------|---------------------|
| 1 | 73.8 | 2141 | 407 | 2 T08732 | hypothetical prote |
| 2 | 627 | 21.6 | 518 | 2 JC4024 | poliovirus recepto |
| 3 | 494 | 17.0 | 467 | 1 HLMSP3 | poliovirus recepto |
| 4 | 470 | 16.2 | 530 | 2 A53437 | poliovirus recepto |
| 5 | 463.5 | 16.0 | 478 | 2 I53960 | PRR2 alpha - human |
| 6 | 449.5 | 15.5 | 538 | 2 I68093 | PRR2 delta - human |
| 7 | 422.5 | 14.6 | 417 | 2 A44194 | poliovirus recepto |
| 8 | 415.5 | 14.3 | 392 | 2 B44194 | poliovirus recepto |
| 9 | 390.5 | 13.5 | 392 | 1 RWHUPD | poliovirus recepto |
| 10 | 390.5 | 13.5 | 417 | 1 RWHUPA | poliovirus recepto |
| 11 | 331.5 | 11.4 | 416 | 2 A54017 | colon carcinoma-as |
| 12 | 230.5 | 7.9 | 764 | 2 A49448 | irregular chiasm C |
| 13 | 216.5 | 7.5 | 4391 | 2 A38096 | perlecan precursor |
| 14 | 201 | 6.9 | 5175 | 2 T20992 | hypothetical prote |
| 15 | 201 | 6.9 | 5198 | 2 T43290 | hemikent in precurs |
| 16 | 198 | 6.8 | 588 | 2 JH0506 | adhesion molecule |
| 17 | 194 | 6.7 | 588 | 2 A45254 | surface glycoprote |
| 18 | 189 | 6.5 | 853 | 1 IJBONC | neural cell adhesi |
| 19 | 187.5 | 6.5 | 274 | 2 A47639 | OX-2 membrane glyc |
| 20 | 187.5 | 6.5 | 7962 | 2 I38346 | elastic titin - hu |
| 21 | 185 | 6.4 | 3707 | 2 S18252 | heparan sulfate pr |
| 22 | 182 | 6.3 | 587 | 2 JH0464 | DM-GRASP precursor |
| 23 | 181.5 | 6.3 | 1896 | 2 T08851 | Down syndrome cell |
| 24 | 178.5 | 6.2 | 847 | 2 JH0371 | B-cell adhesion pr |
| 25 | 174 | 6.0 | 858 | 1 IJRTNC | neural cell adhesi |
| 26 | 173.5 | 6.0 | 761 | 1 IJHUNG | neural cell adhesi |
| 27 | 173 | 6.0 | 637 | 2 B33785 | myelin-associated |
| 28 | 172 | 5.9 | 513 | 2 JC5289 | SHP substrate-1 pr |
| 29 | 171.5 | 5.9 | 822 | 2 B49151 | fibroblast growth |

| | | | | | |
|----|-------|-----|------|----------|--------------------|
| 30 | 171 | 5.9 | 458 | 2 S23969 | cell-adhesion mole |
| 31 | 171 | 5.9 | 582 | 1 ENRT3S | myelin-associated |
| 32 | 171 | 5.9 | 626 | 1 ENRT3 | myelin-associated |
| 33 | 171 | 5.9 | 1259 | 2 A43425 | Bravo/Nr-CAM cell |
| 34 | 169.5 | 5.8 | 1091 | 1 IJCHNL | neural cell adhesi |
| 35 | 169 | 5.8 | 626 | 1 A61084 | myelin-associated |
| 36 | 168 | 5.8 | 765 | 2 C42632 | cell adhesion mole |
| 37 | 168 | 5.8 | 812 | 2 B42632 | cell adhesion mole |
| 38 | 168 | 5.8 | 932 | 2 A42632 | cell adhesion mole |
| 39 | 166.5 | 5.7 | 822 | 2 S19947 | fibroblast growth |
| 40 | 166 | 5.7 | 739 | 2 JN0581 | vascular cell adhe |
| 41 | 165 | 5.7 | 725 | 1 IJMSNG | neural cell adhesi |
| 42 | 165 | 5.7 | 1115 | 1 IJMSNL | neural cell adhesi |
| 43 | 164.5 | 5.7 | 569 | 2 A46462 | T cell activation |
| 44 | 164 | 5.7 | 521 | 2 JCI508 | biliary glycoprote |
| 45 | 163 | 5.6 | 458 | 1 MNMSRI | biliary glycoprote |

ALIGNMENTS

RESULT 1

T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
A:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08732
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: 216474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OTT>
A:Cross-references: UNIPROT:Q9Y412; EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZp566B0846
C:Genetics:
A:Note: DKFZp566B0846.1

Query Match 73.8%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 6.1e-146;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

| | | | |
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| Qy | 143 | SGKYICKAVTEPLGNAQSSTTVTVLVEPTVSLIKGPSLIDGNETVAAICIAATGKPA | 202 |
| Db | 1 | SGKYICKAVTEPLGNAQSSTTVTVLVEPTVSLIKGPSLIDGNETVAAICIAATGKPA | 60 |
| Qy | 203 | HIDWEGDLGEMESTTTTSPNETATIIISQYKLPFTRFARGRRITCVVHPALEKDIRYSFI | 262 |
| Db | 61 | HIDWEGDLGEMESTTTTSPNETATIIISQYKLPFTRFARGRRITCVVHPALEKDIRYSFI | 120 |
| Qy | 263 | LDIQAPEVSVTGYDGNWFGVGRKGNLKCNDANPPPKSVWSRLDGQWPDGLLASDNTL | 322 |
| Db | 121 | LDIQAPEVSVTGYDGNWFGVGRKGNLKCNDANPPPKSVWSRLDGQWPDGLLASDNTL | 180 |
| Qy | 323 | HFVHPLTFNYSGVYICKVTNSLGORSQOKVIYISDPPTTTTLOPTIOWHPSTADIEDLAT | 382 |
| Db | 181 | HFVHPLTFNYSGVYICKVTNSLGORSQOKVIYISDPPTTTTLOPTIOWHPSTADIEDLAT | 240 |
| Qy | 383 | EPKKLPPLSLATIKDDTIATIIASVVGGAFTVLVSVLAGICFYRRRRFRGDFYAKN | 442 |
| Db | 241 | EPKKLPPLSLATIKDDTIATIIASVVGGAFTVLVSVLAGICFYRRRRFRGDFYAKN | 300 |
| Qy | 443 | YIPFSDMQESQIDVLQOQDELSDYPSVKENKPNVNNLIRKDYLEEPEKQMNVENLN | 502 |
| Db | 301 | YIPFSDMQESQIDVLQOQDELSDYPSVKENKPNVNNLIRKDYLEEPEKQMNVENLN | 360 |
| Qy | 503 | RFERPMYYEDLKGMPFVSDHYDENEDDLVSHVDGVSISRREYV | 549 |
| Db | 361 | RFERPMYYEDLKGMPFVSDHYDENEDDLVSHVDGVSISRREYV | 407 |

RESULT 2 JC4024

A:Accession: A53437
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <AOK>
A:Cross-references: UNIPROT:P32507; GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
A:Experimental source: C57/BL6, brain
A>Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 16.2%; Score 470; DB 2; Length 530;
Best Local Similarity 24.8%; Pred. No. 7.1e-26;
Matches 140; Conservative 90; Mismatches 212; Indels 122; Gaps 19;

Qy 30 L L Q P T P P P L L L L F P L L S R L C A L A G P I I V E P H V T A V M G K V S L K C -- L I E V N E T I T 87
Db 6 V L P P S R L S P T L P L L L L Q E T C A Q D V R V R V L P E V R G L G T V E L P C H L L P P T T E R V S 65

Qy 88 Q I S W E K I H G K S S Q T V A V H H P Q Y G F S V Q G E Y -- Q C R V L F ----- K N Y S L A N D A T I L H N I G 139
Db 66 Q V T W O R L D G --- T V V A A F H P S F G V D F P N S Q F S K D R L S F V R A R P E T N A D R L D A T L A F R G L R 122

Qy 140 F S D S G K Y I C K A V T P L G N A Q S S T V T V L V E P ----- T V S L I K G D S L I D G N E T V A A I C I 194
Db 123 V E D G N T C E P A T P N G T R R G V T W L R V I A Q E N H A E A Q E V T I G Q S V ----- A V A R C V 175

Qy 195 A A T K P V A H I D W E G D L G E M E S T T S F P N --- E T A T I I S Q Y K L F P T R F A R G R I T C V V K H P 251
Db 176 S T G C R P P A R I T W I S L G G - B A K D T Q E P G I Q A G T V T I I S R Y S L V P V G R A D G V K V T C R V E H E 234

Qy 252 A L E K D I R Y S F I L D I O Y A P E V S V T G D G N W F V G R K G V N L K C N A D A N P P P F K S V W S R L G Q W 311
Db 235 S F E E P I L L P V T L S V R Y P P E V S I S G Y D D N W Y L G R S E A I L T C D V R N P E P T D Y D W S T T S G V F 294

Qy 312 P D G L A S D N T L H F V H P L T F N Y S G V Y I C K V T N S L G O R S D K V I Y I S D P E T T T L Q P T I Q W H 371
Db 295 P A S A V A Q S Q L - L V H S V D R M W N T F I C A T N A V G T G R A E Q V I L R E S P S T A G A T --- 349

Qy 372 P S T A D I E D L A T E P K K L P P L S T L A T I K D D T I A T I I A S V V G G A L F I V L S V L A G --- I F C Y 428
Db 350 ----- G G I G G I A A I A T A V A G T G I L I C R 374

Qy 429 R R R T F R ----- G D Y F A K N Y I P P S D M Q K E S Q I D V L Q Q E L S Y P D S V K K E N N P 477
Db 375 Q O R K E Q R L Q A D E B E E L E G --- P S Y K P P T P K A K ----- L E E P M P S Q L F T L G A S E H S P 425

Qy 478 V N N I R K D Y L E ----- E P E K T Q N N V N L N R F P M ----- D Y Y E D L 514
Db 426 V --- K T P Y F D A G V S C A D Q E M P R Y H E L P T L E E R S G P L L L G A T G L G P S L L V P P G P N V V E G V 481

Qy 515 K M G M K F V S D E H Y D E N E D D L V S H V D 538
Db 482 S L S L E --- D E E D E E D F L D K I N 502

RESULT 5
I53960
PRR2 alpha - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I53960
R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I53960
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-478 <RES>
A:Cross-references: UNIPROT:Q9UEI6; GB:S79171; NID:g1042202; PID:g1042203
C:Genetics:
C:Superfamily: poliovirus receptor; immunoglobulin homology

F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 16.0%; Score 463.5; DB 2; Length 478;
Best Local Similarity 25.5%; Pred. No. 1.8e-25;
Matches 147; Conservative 76; Mismatches 184; Indels 169; Gaps 20;

Qy 33 P P T P P P L L L L F P L L S R L - C G A L A G P I I V E P H V T A V M G K V S L K C L I --- E V N E T I T Q 88
Db 13 P P T P - - - - - L W P L L L L L L L E T G A Q D V R V Q L P E V R Q L G T V E L P C H L L P P V P G L Y I S L 67

Qy 89 I S W E K I H G K S S - Q T V A V H H P Q Y G F S V Q G E Y Q G -- R V L F ----- K N Y S L N D A T I T L 135
Db 68 V T W Q R P D A P A N H Q N V A A F H P K M G P S P S P K G S R L S F V S A K Q S T G D T E A E L Q D A T L A L 127

Qy 136 H N T G F S D S G K Y I K A V T P P L G N A Q S S T V T V L V E P ----- T V S L I K G D S L I D G N E T 188
Db 128 H G L T V E D G N Y T C E F A T F P K G S V R G M T W L R V I A K P K N Q A B A Q K V T F S Q D P ----- T 178

Qy 189 V A A I C I A A T K P V A H I ----- D W E G D L G E M E S T T S F P N E T A T I I S Q Y K L F P T R F A R G R 242
Db 179 T V A L C I S K E G R P P A R I S W L S S L D W E A K E T Q V S G T L A G --- T V T V T S R F T L V P S G R A D G V 234

Qy 243 R I T C V V K H P A L E K D I R Y S F I L D I O Y A P E V S V T G D G N W F V G R K G V N L K C N A D A N P P P F K S 302
Db 235 T V T C K V E H S F E P A L I P V T L S V R Y P P E V S I S G Y D D N W Y L G R T D A T L S C D V R S N P E T G Y 294

Qy 303 V W S R L D Q W P D G L L A S D N T L H F V H P L T F N Y S G V Y I C K V T N S L G O R S D K V I Y I S D P E T T T 362
Db 295 D W S T T S G T P T S A V A Q S Q L - V I H A V D S L E N T F T F V C T V T N A V G M G R A E Q V I F V R E T P --- 350

Qy 363 T L Q P T Q W H P S T A D I E D L A T E P K K L P P L S T L A T I K D D T I A T I I A S V V G G A L F I V L S V L 422
Db 351 ----- R P R R ----- D V G P L V M G A V G G T L L V L L --- L L 374

Qy 423 A G --- I F C Y R R R T F ----- R G D Y F A K N Y I P P S D M Q K E S 453
Db 375 A G S L A P I L R V R R R R K S P G G A G G S G D G F D P K A Q V L G N G D P V P W T P V P G P M E --- 431

Qy 454 Q I D V L Q Q E L D S Y P D S V K K E N K P V N N I R K D Y L E E P E K T Q N N V N L N R F E R P M D Y Y E D 513
Db 432 ----- P D G ----- K D E E E E E E ----- E K 445

Qy 514 L K M G M K F V S D E H Y D E N E D D L V S H V D S G V I S R R R E W Y V 549
Db 446 A E K G L M L P P P P A L --- E D D M E S Q L D G S L I S R R A V Y V 478

RESULT 6
I68093
PRR2 delta - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I68093
R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I68093
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-538 <RES>
A:Cross-references: UNIPROT:Q92692; GB:S79172; NID:g1042204; PID:g1042205
C:Genetics:
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 15.5%; Score 449.5; DB 2; Length 538;
Best Local Similarity 24.6%; Pred. No. 2.1e-24;
Matches 139; Conservative 91; Mismatches 200; Indels 135; Gaps 20;

Qy 33 P P T P P P L L L L F P L L A F S R L - C G A L A G P I I V E P H V T A V M G K V S L K C L I --- E V N E T I T Q 88
Db 13 P P T P - - - - - L W P L L L L L L L E T G A Q D V R V Q L P E V R Q L G T V E L P C H L L P P V P G L Y I S L 67

N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate proteoglycan
 C;Species: Homo sapiens (man)
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004
 C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
 R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
 J. Biol. Chem. 267, 8544-8557, 1992
 A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membrane, laminin, neural cell adhesion molecules, and epidermal growth factor.
 A;Reference number: A38096; MUID:92235084; PMID:1569102
 A;Accession: A38096
 A;Molecule type: mRNA
 A;Residues: 1-4391 <MUR>
 A;Cross-references: UNIPROT:P98160; GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
 R;Kallunki, P.; Tryggvason, K.
 J. Cell Biol. 116, 559-571, 1992
 A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein with adhesive molecules, and epidermal growth factor.
 A;Reference number: A41736; MUID:92112994; PMID:1730768
 A;Accession: S19256
 A;Molecule type: mRNA
 A;Residues: 1-57, 'D', '59-434', 'A', '436', 'FL', '438-449', 'Q', '451-502', 'A', '503-792', 'K', '794-908', 'R', '910-979', 'H', '2981-2994', 'G', '2996-3167', 'T', '3169-3240', 'R', '3242-3426', 'R', '3428-3631', 'Q', '3633-3634', 'R', '3635-3636', 'G', '3637-3638', 'T', '3639-3640', 'R', '3641-3642', 'R', '3643-3644', 'R', '3645-3646', 'R', '3647-3648', 'R', '3649-3650', 'R', '3651-3652', 'R', '3653-3654', 'R', '3655-3656', 'R', '3657-3658', 'R', '3659-3660', 'R', '3661-3662', 'R', '3663-3664', 'R', '3665-3666', 'R', '3667-3668', 'R', '3669-3670', 'R', '3671-3672', 'R', '3673-3674', 'R', '3675-3676', 'R', '3677-3678', 'R', '3679-3680', 'R', '3681-3682', 'R', '3683-3684', 'R', '3685-3686', 'R', '3687-3688', 'R', '3689-3690', 'R', '3691-3692', 'R', '3693-3694', 'R', '3695-3696', 'R', '3697-3698', 'R', '3699-3700', 'R', '3701-3702', 'R', '3703-3704', 'R', '3705-3706', 'R', '3707-3708', 'R', '3709-3710', 'R', '3711-3712', 'R', '3713-3714', 'R', '3715-3716', 'R', '3717-3718', 'R', 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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:34:02 ; Search time 81.4368 Seconds
(without alignments)
3452.143 Million cell updates/sec

Title: US-09-972-268-6
Perfect score: 2901
Sequence: 1 MARTLRPSPLCPGGKAQLS.....EDDLVSHVDSVISRREWYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|------------|--------------------|
| 1 | 2901 | 100.0 | 549 | 2 | Q9NQ53 | Q9NQ53 homo sapien |
| 2 | 2721 | 93.8 | 549 | 2 | Q9JLB9 | Q9JLB9 mus musculu |
| 3 | 2677 | 92.3 | 549 | 2 | Q9D006 | Q9D006 mus musculu |
| 4 | 2141 | 73.8 | 407 | 2 | Q9Y412 | Q9Y412 homo sapien |
| 5 | 1872 | 64.5 | 366 | 2 | Q6NV23 | Q6NV23 homo sapien |
| 6 | 1814.5 | 62.5 | 510 | 2 | Q9JLB8 | Q9JLB8 mus musculu |
| 7 | 1809.5 | 62.4 | 438 | 2 | Q9JLB7 | Q9JLB7 mus musculu |
| 8 | 1629 | 56.2 | 304 | 2 | Q9BVA9 | Q9BVA9 homo sapien |
| 9 | 1235 | 42.6 | 267 | 2 | Q8NC05 | Q8NC05 homo sapien |
| 10 | 659.5 | 22.7 | 515 | 1 | PVR1 MOUSE | Q9Jkf6 mus musculu |
| 11 | 653.5 | 22.5 | 515 | 2 | Q6P9M9 | Q6P9M9 mus musculu |
| 12 | 649.5 | 22.4 | 517 | 1 | PVR1 HUMAN | Q15223 homo sapien |
| 13 | 641.5 | 22.1 | 515 | 1 | PVR1_PIG | Q9gl16 sus scrofa |
| 14 | 544 | 18.8 | 510 | 2 | Q96NY8 | Q96NY8 homo sapien |
| 15 | 543 | 18.7 | 510 | 2 | Q96K15 | Q96K15 homo sapien |
| 16 | 542 | 18.7 | 101 | 2 | Q8WVU4 | Q8WVU4 homo sapien |
| 17 | 534.5 | 18.4 | 295 | 2 | Q9ERF5 | Q9ERF5 mesocricetu |
| 18 | 528 | 18.2 | 298 | 2 | Q9GL74 | Q9GL74 cercopithec |
| 19 | 526.5 | 18.1 | 295 | 2 | Q9GL75 | Q9GL75 bos taurus |
| 20 | 506 | 17.4 | 508 | 2 | Q8CED8 | Q8CED8 mus musculu |
| 21 | 506 | 17.4 | 508 | 2 | Q8R007 | Q8R007 mus musculu |
| 22 | 504 | 17.4 | 463 | 2 | Q6GLJ2 | Q6GLJ2 xenopus lae |
| 23 | 502.5 | 17.3 | 464 | 2 | Q6GL25 | Q6GL25 xenopus tro |
| 24 | 496 | 17.1 | 467 | 2 | Q8CF22 | Q8CF22 mus musculu |
| 25 | 494 | 17.0 | 467 | 2 | Q9IVT9 | Q9IVT9 mus musculu |
| 26 | 493.5 | 17.0 | 483 | 2 | Q9DBF8 | Q9DBF8 mus musculu |
| 27 | 474 | 16.3 | 530 | 2 | Q80XJ5 | Q80XJ5 mus musculu |
| 28 | 470 | 16.2 | 530 | 1 | PVR2 MOUSE | P32507 mus musculu |
| 29 | 449.5 | 15.5 | 538 | 1 | PVR2 HUMAN | Q92692 homo sapien |
| 30 | 432 | 14.9 | 449 | 2 | Q9UE16 | Q9UE16 homo sapien |
| 31 | 423.5 | 14.6 | 400 | 2 | Q8HY16 | Q8HY16 cebus apell |

32 422.5 14.6 417 1 PVR_CERAE
33 413.5 14.3 412 2 Q9RIE1
34 408.5 14.1 412 2 Q63611
35 400.5 13.8 401 2 Q08835
36 393 13.5 408 2 Q91WP1
37 391.5 13.5 412 2 Q8HY14
38 391 13.5 408 2 Q8K094
39 390.5 13.5 417 1 PVR_HUMAN
40 390 13.4 408 2 Q8BVF6
41 381.5 13.2 403 2 Q8HY15
42 346 11.9 415 2 Q60977
43 342.5 11.8 476 2 Q6AYP5
44 336.5 11.6 456 2 Q8R5M8
45 334.5 11.5 442 2 Q9BY67

ALIGNMENTS

RESULT 1

Q9NQ53 ID Q9NQ53 PRELIMINARY; PRT; 549 AA.
AC Q9NQ53;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;
Query Match 100.0%; Score 2901; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 8.2e-208;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MARTLRPSPLCPGGKAQLSSALLGAGLLQLPPTPPPLLLLPFLRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETTQISWEKHGKSQTAVHHQYGFSGVQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETTQISWEKHGKSQTAVHHQYGFSGVQGR 120
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Db 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGORSDOKVIYISDPT 360

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QY 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPPLSLTATIKDDTIATIIASVVGGALFVLVS 420
Db 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPPLSLTATIKDDTIATIIASVVGGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELSDYSPDSVKKENKPNVNN 480
Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELSDYSPDSVKKENKPNVNN 480
QY 481 LIRKDYLEPEKTOQNNVNNLNRFRPMDYIEDLKMGMKFPVSDHEDNEDDLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVNNLNRFRPMDYIEDLKMGMKFPVSDHEDNEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 2
Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 60582 MW; 5492C9ABB472F185 CRC64;

Query Match 93.8%; Score 2721; DB 2; Length 549;
Best Local Similarity 92.98; Pred. No. 2.2e-194;
Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 MARTLRSPICPGGKQAQLSSASILLGALLLQPPPTPPPLLLLPPLLLFSLRCGALAGPI 60
Db 1 MARTPGAPICPGGKQAQLSSAPPAAGLLLPAPTPPPLLLLPPLLLFSLRCGALAGSI 60
QY 61 IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGR 120
Db 61 IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTVLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTVLVEPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAACVAATGKPVQAIDWEGDLGEMESTTTSPNETATIVSQYKLPPTFRAR 240

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QY 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANPPPF 300
QY 301 KSVWSRLDQWPGDLLASNTLHFVHPLTFNYSVVYICKVTNSLQSGRSQDKVIYISDPPT 360
Db 301 KSVWSRLDQWPGDLLASNTLHFVHPLTFNYSVVYICKVTNSLQSGRSQDKVIYISDPPT 360
QY 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPPLSLTATIKDDTIATIIASVVGGALFVLVS 420
Db 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPPLSLTATIKDDTIATIIASVVGGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELSDYSPDSVKKENKPNVNN 480
Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELSDYSPDSVKKENKPNVNN 480
QY 481 LIRKDYLEPEKTOQNNVNNLNRFRPMDYIEDLKMGMKFPVSDHEDNEDDLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVNNLNRFRPMDYIEDLKMGMKFPVSDHEDNEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 3
Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610301B19 product:poliovirus receptor-related
DE 3, full insert sequence.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazana M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Receptor.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

Query Match 92.3%; Score 2677; DB 2; Length 549;
Best Local Similarity 91.4%; Pred. No. 4.3e-191;
Matches 502; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGGKQAQLSSASLLGALLLOPPTPPPLLLPLLLFSLRCGALAGPI 60
Db 1 MARTFGAPLCPGGKQAQLSSAFPAPAGLLLPATPPPLLLPLLLFSLRCGALAGSI 60
Qy 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKIHGSKSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKIHGSKSTQVAVHHPOYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDS 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDS 180
Qy 181 LIDGNEVVAICIAATGKPAVHIDWEGDLGEMSTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVHKPALEKDIRYSFI 240
Db 181 SIDGNEVVAICVSSSTGKPAQIDWEGDLGERFSTISFNETATIVSQYELFPPTPAR 240
Qy 241 GRRITCVVHKPALEKDIRYSFILDIQVAPESVTVGDNWFGKGNLKNADANPPPF 300
Db 241 GRRITCVVHKPALEKDIRYSFILDIQVAPESVTVGDNWFGKGNLKNADANPPPF 300
Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDQKVIISDPPT 360
Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNSLQGRSDQKVIISDPPT 360
Qy 361 TTTTLOPTIOWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFVLVLS 420
Db 361 TTTTLOPTIOWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFVLVLS 420

SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 73.8%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 2.9e-151;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 143 SGKVIKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDSLIDGNETVAAICIAATGKEVA 202
Db 1 SGKVIKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDSLIDGNETVAAICIAATGKEVA 60
Qy 203 HIDWEGDLGEMSTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVHKPALEKDIRYSFI 262
Db 61 HIDWEGDLGEMSTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVHKPALEKDIRYSFI 120
Qy 263 LDIOYAPEVSVTVGDNWFGKGNLKNADANPPPFKSVMSRLDQWPDGGLASDNTL 322
Db 121 LDIOYAPEVSVTVGDNWFGKGNLKNADANPPPFKSVMSRLDQWPDGGLASDNTL 180
Qy 323 HFVHPLTFNYSGVYICKVNSLQGRSDQKVIISDPPTTTTLOPTIOWHPSTADIEDLAT 382
Db 181 HFVHPLTFNYSGVYICKVNSLQGRSDQKVIISDPPTTTTLOPTIOWHPSTADIEDLAT 240
Qy 383 EPKLPPLSTLATIKDDTIATIIASVVGALFVLVSVLAGIFCYRRRRTRFRGDYFAKN 442
Db 241 EPKLPPLSTLATIKDDTIATIIASVVGALFVLVSVLAGIFCYRRRRTRFRGDYFAKN 300
Qy 443 YIPSDMKQESQIDVLQODELSDYSPSVKKNKPNVNLTKDYLEBPEKTMNNVENLN 502
Db 301 YIPSDMKQESQIDVLQODELSDYSPSVKKNKPNVNLTKDYLEBPEKTMNNVENLN 360
Qy 503 RFERPMYDIEDLKMGKMFVSDHEVDENEDDLVSHVDGVSISRREWYV 549
Db 361 RFERPMYDIEDLKMGKMFVSDHEVDENEDDLVSHVDGVSISRREWCV 407

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RESULT 5
Q6NVZ3 ID Q6NVZ3 PRELIMINARY; PRT; 366 AA.
AC 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PVRL3 protein.
GN Name=PVRL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McWeeny P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067808; AA467808.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 366 AA; 39722 MW; 591D0A4687C630BA CRC64;

Query Match 64.5%; Score 1872; DB 2; Length 366;
Best Local Similarity 99.7%; Pred. No. 3e-131;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARTLRSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFRLCGALAGPI 60
Db 1 MARTLRSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFRLCGALAGPI 60

Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETTIQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVGKNSVLSKCLIEVNETTIQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGGNETVAAICAAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTPFAR 240
Db 181 LIDGGNETVAAICAAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTPFAR 240

Qy 241 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 300
Db 241 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 300

Qy 181 LIDGGNETVAAICAAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTPFAR 240
Db 181 LIDGGNETVAAICAAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTPFAR 240

Qy 241 GRRITCVVHPALEKDIRYSFILDIOYAVEPSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOYAVEPSVTGYDGNWFGVGRKGNLKNADANPPPF 300

Qy 361 TTTTLOPTIQWHPSTADIEDLATBPKKLPFPLSTLATIKDDTIATIIATISVVGALFIVLVS 420
Db 361 TTTTLOPTIQWHPSTADIEDLATBPKKLPFPLSTLATIKDDTIATIIATISVVGALFIVLVS 420
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Db 361 TQT-----SSIA-----VAGAVIGALVLFIT 383
Qy 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMOK---ESQIDVLOQDEL-----DSTPDSVKK 472
Db 384 VFVTLLTPRKK--RPSYLDKVIDLPPTHKPPVVEERIPSLPQKDLGQTHLPLQTOF 441
Qy 473 ENK-----NPVNNLRKDYLEBEKT-QWNNVENLNRFERPMDYVEDLKMGMKFVSDHY 526
Db 442 KEKGGGLQPSGPISRPFYEDSTQMEDGTQKMCPLYSQWCHQDRSPR-----QHH 494
Qy 527 DENEDDLVSHVDSGISREWYV 549
Db 495 PRNPERL-----YINPREHYV 510

RESULT 7
Q9JLB7
ID Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN Name=Pvr13;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoch-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416B5B02FEF CRC64;

Query Match 62.4%; Score 1809.5; DB 2; Length 438;
Best Local Similarity 76.2%; Pred. No. 1.8e-126;
Matches 356; Conservative 25; Mismatches 43; Indels 43; Gaps 5;

Qy 1 MARTLRSPCLPGGKQALSSASLIGALLQPTPPPLLLLPLLLFSLRCLGALAGPI 60
Db 1 MARTPGAPLCPGGKQALSSAFAAAGLLLPAPTPPLLLLPLLLFSLRCLGALAGSI 60
Qy 61 IVEPHVAVGKNVSLKCLIEVNETITQISKEKHGKSSQTVAVHHQYGFSGVQYQGR 120
Db 61 IVEPHVAVGKNVSLKCLIEVNETITQISKEKHGKSSQTVAVHHQYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDATITLHNGFSDSGYICKAVTFPLGNAQSSTTVTLVPEVTSLIKGPDS 180
Db 121 VLFKNYSLNDATITLHNGFSDSGYICKAVTFPLGNAQSSTTVTLVPEVTSLIKGPDS 180
Qy 181 LIDGNETVAAICAAATGKPAHVDWEGDLGEMESTTSPFNETATIIISQYKLPFTRPAR 240
Db 181 LIDGNETVAAVCAATGKPAQVDWEGDLGEMESTTSPFNETATIVSQYKLPFTRPAR 240
Qy 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300
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Db 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300
Qy 301 KSVMSRLDQGWPDGGLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIISDPPT 360
Db 301 KSVMSRLDQGWPDGGLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIISDPL 360
Qy 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLPLSTLATIKDDTIATIIASVVGALFVLVS 420
Db 361 TQT-----SSIA-----VAGAVIGALVLFIT 383
Qy 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMOK---ESQIDVLOQDEL 463
Db 384 VFVTLLTPRKK--RPSYLDKVIDLPPTHKPPVVEERIPSLPQKDL 428

RESULT 8
Q9BVA9
ID Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nectin 3; DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUR=Cervix;
RA Strausberg R.;
RL Submitted (DSC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 56.2%; Score 1629; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.2e-113;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CVVKGHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPFKSVMS 305
Db 1 CVVKGHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPFKSVMS 60
Qy 306 RLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIISDPPTTTLQ 365
Db 61 RLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIISDPPTTTLQ 120
Qy 366 PTIQWHPSTADIEDLATEPKLPPLPLSTLATIKDDTIATIIASVVGALFVLVSLAGI 425
Db 121 PTIQWHPSTADIEDLATEPKLPPLPLSTLATIKDDTIATIIASVVGALFVLVSLAGI 180
Qy 426 FCYRRRTFRGDYFAKNYIPPSDMOKESQIDVLOQDELDSYPSVKKNKPNVNLIRKD 485
Db 181 FCYRRRTFRGDYFAKNYIPPSDMOKESQIDVLOQDELDSYPSVKKNKPNVNLIRKD 240
Qy 486 YLEPEKTOVNNVENLNRFERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDSGISRR 545
Db 241 YLEPEKTOVNNVENLNRFERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDSGISRR 300
Qy 546 EWYV 549
Db 301 EWYV 304

RESULT 9
Q8NC05
ID Q8NC05 PRELIMINARY; PRT; 267 AA.
AC Q8NC05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

```
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwavanagi T., Ninomiya K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
KW Receptor.
SQ
Sequence 267 AA; 29253 MW; 4F4648A1BA0C451 CRC64;

Query Match 42.6%; Score 1235; DB 2; Length 267;
Best Local Similarity 96.0%; Pred. No. 6.8e-84;
Matches 242; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 41 LLEFPLL-LFSRLCGALAGPIIIEPHVTAWGNVSLKCLIEVNETITQISWEKIHGKS 98
DB 16 LRLGRLPRSGFNPRALAGPIIIEPHVTAWGNVSLKCLIEVNETITQISWEKIHGKS 75

QY 99 SQTVAHHPOYGSVOGEYQGRVLFKNYSNDATITLHNTGFSDSGKYICKAVTFPLGNA 158
DB 76 SQTVAHHPOYGSVOGEYQGRVLFKNYSNDATITLHNTGFSDSGKYICKAVTFPLGNA 135

QY 159 QSSTTVTLVPEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 218
DB 136 QSSTTVTLVPEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 195

QY 219 SFPNETATIIISQYKLPFRFARGRRITCVVVKHPALEKDIRYSPILDIQYAPESVVTGYDG 278
DB 196 SFPNETATIIISQYKLPFRFARGRRITCVVVKHPALEKDIRYSPILDIQYAPESVVTGYDG 255

QY 279 NWFVGGKGVNLK 290
DB 256 NWFVGGKGVNLK 267

RESULT 10
PVRL MOUSE
ID PVRL1_MOUSE STANDARD; PRT; 515 AA.
AC Q9JKE6; Q9JEL5; Q9J117;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1).
GN Names=Pr1; Synonyms=HvEC, Pr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2043378; PubMed=10781093; DOI=10.1073/pnas.97.9.4867;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
RA Lecoq E., Dubreuil P., Campadelli-Piime G.;
RT "The murine homolog of human nectin delta serves as a species
RT nonspecific mediator for entry of human and animal alpha herpesviruses
RT in a pathway independent of detectable binding to gp.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RX DOI=10.1128/JVI.74.24.11773-11781.2000;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha
RT (HvEC) in sequence and activity as a glycoprotein D receptor for
RT alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPR1), a herpesvirus receptor, is expressed in the
RT floor plate during embryogenesis, suggesting a role in neural
RT development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Probably involved in cell adhesion. Receptor for
CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
CC cells.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
EMBL; AF239762; AAF60333.1; -.
EMBL; AF270977; AAF76195.1; -.
EMBL; AF297665; AAG22808.1; -.
DR HSSP; Q05793; 1GL4.
DR MGD; MGI:1926483; Pvr11.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR007110; Ig-Like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 515 Poliovirus receptor related protein 1.
FT DOMAIN 31 354 Extracellular (Potential).
FT TRANSMEM 355 375 Potential.
FT DOMAIN 376 515 Cytoplasmic (Potential).
FT DOMAIN 31 141 Ig-like V-type.
FT DOMAIN 145 243 Ig-like C2-type 1.
FT DOMAIN 247 334 Ig-like C2-type 2.
FT DOMAIN 436 442 Poly-Glu.
FT DOMAIN 443 447 Poly-Gly.
FT DISULFID 51 124 By similarity.
FT DISULFID 172 226 By similarity.
FT DISULFID 269 316 By similarity.
FT CARBOHYD 36 36 N-linked (GLNAC... ) (Potential).
FT CARBOHYD 72 72 N-linked (GLNAC... ) (Potential).
FT CARBOHYD 139 139 N-linked (GLNAC... ) (Potential).
FT CARBOHYD 202 202 N-linked (GLNAC... ) (Potential).
FT CARBOHYD 286 286 N-linked (GLNAC... ) (Potential).
FT CARBOHYD 297 297 N-linked (GLNAC... ) (Potential).
FT CARBOHYD 332 332 N-linked (GLNAC... ) (Potential).
FT CONFLICT 138 138 L -> P (in Ref. 1).
FT CONFLICT 165 165 N -> D (in Ref. 1).
FT CONFLICT 342 342 P -> Pp (in Ref. 2).
FT CONFLICT 428 428 S -> G (in Ref. 3).
SQ SEQUENCE 515 AA; 57064 MW; FFF608B5FFB7A0F CRC64;
Query Match 22.7%; Score 659.5; DB 1; Length 515;
Best Local Similarity 32.5%; Pred. No. 1.6e-40;
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Matches 170; Conservative 83; Mismatches 175; Indels 95; Gaps 18;

Qy 71 GKNVSLKCLIE--VNETITQISWEKTHGKSSQTVAVHHPQYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLSPVKITQVTWQKASNGSKNNAIYPTMGVSUVPPEYKRVFLRPS 103
Qy 128 LNDATITLHNGFSDSGYICKAVTFPLGNAQSSSTVTLVLEPTVSLIKGPDSDLIG--- 184
Db 104 FIDGTIRLSGLEDEGMYCEPATFTGNRESQNLNLTVMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTSPNETATIIISQYKLFPTFRFARGR 242
Db 163 QDNKVLVATCTSANGKPPSAVSWETRLKGEAEYQEIIRNPNGTIVTISRVLVPSREAHQ 222
Qy 243 RITCVKHPALEKDIRVSFILDIOYAPEVSVTGDNWVFCRKGKVNLCNADANPPFPKS 302
Db 223 SLACIVNY-HLDR-FRESLTINVQYEPVEITIEGDNWYIQTVDKLTCKADANPPATEY 280
Qy 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQKVIYISDPPTTT 362
Db 281 HWTTLNSLPGVEAQNRITLFFRGPIYSLAGTYICEATNPIGTRSGQVEVNIETFPYTP 340
Qy 363 TLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGGFALFVLVSVL 422
Db 341 TPE-----HGRRAG-----QMP-----TAIGGVAGSVLLVLI-VV 370
Qy 423 AGIF-CYRRRTFRGDYFAKNYI-----PPSDMQESQIDVLQDELDYSY 466
Db 371 GGIIVALLRRRHTFKGDYSTKKHYGVNGYSKAGIPQHHPP--MAQNLQ-----Y 417
Qy 467 PDSVKKENK-NPVNNLIRKDYLBEPKTKQNNV-----NLNRFER 506
Db 418 PDSDDKKKAPLGG-----SSYESEEEEGGGGKRGVGGPHPKYDEDAKRPYFTVDEAEA 474
Qy 507 PMDYEDLKMGMKFPVSDEHYDENDDLVSHVDGVSISRREWYV 549
Db 475 RODGYGRTLGYYQ--DPEQLDLAENMVSNQDGSFISKEMYV 515

RESULT 11

Q6P9M9 PRELIMINARY; PRT; 515 AA.

AC Q6P9M9

DT 05-JUN-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Poliovirus receptor-related 1.

GN Name=Pvrl1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RK MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RN RP
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC60694; AA60694.1; -;
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;

Query Match 22.5%; Score 653.5; DB 2; Length 515;
Best Local Similarity 32.3%; Pred. No. 4.4e-40;
Matches 169; Conservative 83; Mismatches 176; Indels 95; Gaps 18;

Qy 71 GKNVSLKCLIE--VNETITQISWEKTHGKSSQTVAVHHPQYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLSPVKITQVTWQKASNGSKNNAIYPTMGVSUVPPEYKRVFLRPS 103
Qy 128 LNDATITLHNGFSDSGYICKAVTFPLGNAQSSSTVTLVLEPTVSLIKGPDSDLIG--- 184
Db 104 FIDGTIRLSGLEDEGMYCEPATFTGNRESQNLNLTVMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTSPNETATIIISQYKLFPTFRFARGR 242
Db 163 QDNKVLVATCTSANGKPPSAVSWETRLKGEAEYQEIIRNPNGTIVTISRVLVPSREAHQ 222
Qy 243 RITCVKHPALEKDIRVSFILDIOYAPEVSVTGDNWVFCRKGKVNLCNADANPPFPKS 302
Db 223 SLACIVNY-HLDR-FRESLTINVQYEPVEITIEGDNWYIQTVDKLTCKADANPPATEY 280
Qy 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQKVIYISDPPTTT 362
Db 281 HWTTLNSLPGVEAQNRITLFFRGPIYSLAGTYICEATNPIGTRSGQVEVNIETFPYTP 340
Qy 363 TLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGGFALFVLVSVL 422
Db 341 TPE-----HGRRAG-----QMP-----TAIGGVAGSVLLVLI-VV 370
Qy 423 AGIF-CYRRRTFRGDYFAKNYI-----PPSDMQESQIDVLQDELDYSY 466
Db 371 GGIIVALLRRRHTFKGDYSTKKHYGVNGYSKAGIPQHHPP--MAQNLQ-----Y 417
Qy 467 PDSVKKENK-NPVNNLIRKDYLBEPKTKQNNV-----NLNRFER 506
Db 418 PDSDDKKKAPLGG-----SSYESEEEEGGGGKRGVGGPHPKYDEDAKRPYFTVDEAEA 474
Qy 507 PMDYEDLKMGMKFPVSDEHYDENDDLVSHVDGVSISRREWYV 549
Db 475 RODGYGRTLGYYQ--DPEQLDLAENMVSNQDGSFISKEMYV 515

RESULT 12

PVR1 HUMAN
ID PVR1 HUMAN STANDARD; PRT; 517 AA.
AC Q15223; O75465; Q9HBE6; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD111 antigen).
OS Name=PVRL1; Synonyms=HVEC, PRR1;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G;
RA Lopez M., Eberle F., Mattei M.-G., Gabart J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "cDNA characterization and chromosomal localization of a gene related
RT to the poliovirus receptor gene.";
RL Gene 155:261-265(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127; DOI=10.1126/science.280.5369.1618;
RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
RA Spear P.G.;
RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
RT protein 1 and poliovirus receptor.";
RL Science 280:1618-1620(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
RA Campadelli-Fiume G., Dubreuil P.;
RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
RT nectin1 (or pr1-HIGR-HVEC) modulates positively and negatively
RT susceptibility to hsv infection.";
RL J. Virol. 75:5684-5691(2001).
RN [4]
RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
RX MEDLINE=20323396; PubMed=10932188; DOI=10.1038/78119;
RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
RA Helms J.A., Spritz R.A.;
RT "Mutations of PVRL1, encoding a cell-cell adhesion
RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
RT dysplasia.";
RL Nat. Genet. 25:427-430(2000).
CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gpD).
CC -1- FUNCTION: Probably involved in cell adhesion. Receptor for
CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
CC cells.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoform gamma).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=Delta;
CC IsoId=Q15223-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
CC Name=Gamma;
CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
CC -1- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
CC ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is
CC responsible for allelic forms known as Margarita island ectodermal
CC dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930.g.htm".
CC -----
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or send an email to license@isb-sib.ch.
CC -----
CC EMBL; X76400; CAAS3980.2; ALT_INIT.
DR EMBL; AF060231; AAC23798.1; -.
DR EMBL; AY029539; AAK3124.1; -.
DR EMBL; AF252867; AAG16648.1; -.
DR EMBL; AF196768; AAG16648.1; JOINED.
DR EMBL; AF196769; AAG16648.1; JOINED.
DR EMBL; AF196770; AAG16648.1; JOINED.
DR EMBL; AF196771; AAG16648.1; JOINED.
DR EMBL; AF196772; AAG16649.1; -.
DR EMBL; AF196768; AAG16649.1; JOINED.
DR EMBL; AF196769; AAG16649.1; JOINED.
DR EMBL; AF196770; AAG16649.1; JOINED.
DR EMBL; AF196771; AAG16649.1; JOINED.
DR EMBL; AF196772; AAG16649.1; JOINED.
DR EMBL; AF196773; AAG16649.1; JOINED.
DR EMBL; HGNC:9706; PVRL1.
DR MIM; 600644; -.
DR MIM; 225000; -.
DR MIM; 225060; -.
DR GO; GO:0005912; C:adherens junction; NAS.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0048718; P:viral entry; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Alternative splicing; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 517 Poliovirus receptor related protein 1.
FT DOMAIN 31 355 Extracellular (Potential).
FT TRANSMEM 356 376 Potential.
FT DOMAIN 377 517 Cytoplasmic (Potential).
FT DOMAIN 31 141 Ig-like V-type.
FT DOMAIN 149 238 Ig-like C2-type 1.
FT DOMAIN 247 334 Ig-like C2-type 2.
FT DOMAIN 437 444 Poly-Gly.
FT DOMAIN 445 449 Poly-Gly.
FT DISULFID 51 124 By similarity.
FT DISULFID 172 226 By similarity.
FT DISULFID 269 316 By similarity.
FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 286 286 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 332 332 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 335 352 EPPYTPSPPEHGRAGPV -> AFCQLIYVPGKGRTRARMF
FT (in isoform Gamma).
FT FTId=VSP_002624.
FT VARSPPLIC 353 517 Missing (in isoform Gamma).
FT FTId=VSP_002625.
FT VARSPPLIC 336 458 FPVTPSPPEHGRAGPVPTAIIGVAGSILLVIVGGIVV
ALRRRSHTEKGDYSTKKHYVNGYSKAGIQQHPHPMAONLQ
YFDDSDDEKAGPLGSSSEEEBEGGGGKVGKGGPH
-> KPRPQGLGAARLAVFLVAVLAVLAVLFFVLYNRQ
KSPQPDAGTDQPLSKQPEPSRQSSSLVPEDIQVHLD
QKSPQQEEDDLQKLSLQPPYDLGVSPSPYHPSVRRTPERG
ECP (in isoform Alpha).
FT FTId=VSP_002626.
FT VARSPPLIC 459 517 Missing (in isoform Alpha).
FT FTId=VSP_002627.
SQ SEQUENCE 517 AA; 57158 MW; DF34C8AEC993EB6D CRC64;
Query Match 22.4%; Score 649.5; DB 1; Length 517;


```

QY 498 VENLNFRPFMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVIGRREWYV 549
Db 468 --TVDAEARDQGYGRTIGYQV--DPEQLDLAENWVSQNDGSFISKWYV 515

RESULT 14
QY 96NY8 PRELIMINARY; PRT; 510 AA.
ID Q96NY8
AC Q96NY8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Nectin 4 (pVRL4 protein).
GN Name-pVRL4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21560925; PubMed=11544254; DOI=10.1074/jbc.M103810200;
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RT "Nectin4/PRR4, a new afadin-associated member of the nectin family
that trans-interacts with nectin1/PRR1 through V domain interaction.";
RL J. Biol. Chem. 276:43205-43215 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smallos J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF426163; AAL23958.1; -
DR ENBL; BC010423; AAL10423.1; -
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 510 AA; 55454 MW; DCF5E1D794F227FA CRC64;

Query Match 18.8%; Score 544; DB 2; Length 510;
Best Local Similarity 28.4%; Pred. No. 6.4e-32;
Matches 149; Conservative 85; Mismatches 213; Indels 78; Gaps 15;

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Db 12 PEAWLLLLLLASFTGRCP--AGELETSDVVTVVLGGQAKLPCYRGDSGEQVQVAVAR 69

QY 94 IH-GKSSQTVAVHHPQYGFSGYQGRVFKFNYSLN--DATITLHNGFSDSGKYICKA 150
Db 70 VDAGEGAQELALLHSGYGLHVSYPAYEGRVQPPPPRNPDLGSLVLLNAVQADEGEYCRV 129

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QY 271 VSVTVGYDGN--WFGVRGKGNLKNADANPPFKSVMSRLDGOWPDGGLLASDNLHFWHPL 328
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QY 495 WNNVNLNFRPFMDYY-----EDLKMGMKFVSDHYDEN 529
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AC Q96K15
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musahino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihara K., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata R., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

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"Complete sequencing and characterization of 21,243 full-length human

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RT CDNA#";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK027753; BAB5344.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_Like; 3.
KW Receptor.
SQ SEQUENCE 510 AA; 55382 MW; 9B68CD50F086429E CRC64;

Query Match      18.7%; Score 543; DB 2; Length 510;
Best Local Similarity 28.4%; Pred. No. 7.6e-32;
Matches 149; Conservative 85; Mismatches 213; Indels 78; Gaps 15;

Qy 36 PPPLLLLPFLLSRLCALAGPIIVPHPTAVMGKNSLKCLI--EVNETITQISWEK 93
Db 12 PEAWLLLLLLASTGRCP--AGELGTSDDVVTVVLGQDAKLPCTFYRGDSGEQGVQVAWAR 69

Qy 94 IH-QKSSQTVAVHHPQVGFSGVQGRVLFKNYSLN--DATITLHNIIGFSDSGKYICKA 150
Db 70 VDAGEGAQELALLHSKYLGHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVAQADEGEYECRV 129

Qy 151 VTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGNETVAAICAAATGKPVAHIDWEGDL 210
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Job time : 82.4368 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 22.914 Seconds
(without alignments)
1782.508 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 2901

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 649.5 | 22.4 | 517 | 4 | US-09-723-368-4 |
| 3 | 627 | 21.6 | 518 | 4 | US-09-919-172-20 |
| 4 | 566 | 19.5 | 458 | 4 | US-09-435-956A-1 |
| 5 | 469.5 | 16.2 | 522 | 4 | US-09-949-016-7563 |
| 6 | 463 | 16.0 | 479 | 4 | US-09-723-368-2 |
| 7 | 463 | 16.0 | 479 | 4 | US-09-949-016-6278 |
| 8 | 394.5 | 13.6 | 456 | 4 | US-09-949-016-7564 |
| 9 | 391 | 13.5 | 408 | 3 | US-09-724-864-62 |
| 10 | 390.5 | 13.5 | 417 | 4 | US-09-949-016-6729 |
| 11 | 335.5 | 11.6 | 442 | 4 | US-09-778-510-20 |
| 12 | 335.5 | 11.6 | 442 | 4 | US-09-930-803-1 |
| 13 | 333.5 | 11.5 | 440 | 4 | US-09-866-028-61 |
| 14 | 333.5 | 11.5 | 440 | 4 | US-09-944-457-61 |
| 15 | 335.5 | 11.2 | 423 | 4 | US-09-778-510-22 |
| 16 | 263 | 9.1 | 444 | 2 | US-08-659-984A-5 |
| 17 | 263 | 9.1 | 444 | 3 | US-08-660-531-5 |
| 18 | 255.5 | 8.8 | 421 | 2 | US-08-659-984A-1 |
| 19 | 255.5 | 8.8 | 421 | 3 | US-08-660-531-1 |
| 20 | 249 | 8.6 | 398 | 4 | US-09-778-510-4 |
| 21 | 243 | 8.4 | 398 | 4 | US-09-778-510-6 |
| 22 | 243 | 8.4 | 398 | 4 | US-09-907-794A-84 |
| 23 | 243 | 8.4 | 398 | 4 | US-09-905-125A-84 |
| 24 | 243 | 8.4 | 398 | 4 | US-09-902-775A-84 |
| 25 | 243 | 8.4 | 398 | 4 | US-09-906-700-84 |
| 26 | 243 | 8.4 | 398 | 4 | US-09-903-603A-84 |
| 27 | 243 | 8.4 | 398 | 4 | US-09-904-920A-84 |

ALIGNMENTS

RESULT 1

US-09-949-016-11380
; Sequence 11380, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11380

; LENGTH: 514

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-11380

Query Match 22.4%; Score 649.5; DB 4; Length 514;

Best Local Similarity 31.9%; Pred. No. 1e-51;

Matches 167; Conservative 80; Mismatches 182; Indels 95; Gaps 17;

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| Db | 160 | QDDKVLVATCTSANGKPPSVVSWETRLKGEAYQEIIRNPNGTIVTISRILVPSREAHQ | 219 |
| Qy | 243 | RITCVVHKPALEKDIRYSFILDIQYAPSVSVTGVDGNWFGVRKGVNLKCNADANPPPKS | 302 |
| Db | 220 | SLACIVNHYM--DRFKESLTINVOYEPEVTIEGFGNWLQRMVMDVKLTCKADANPPATEY | 277 |
| Qy | 303 | VWSRLDGQWPDGLIASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKQVIYISDPPTTT | 362 |
| Db | 278 | HWTTLNGLPKGVFAQNRTLFFKGPINYSLAGTYICENTNPIGTRSGQVEVNIETFPYT- | 336 |
| Qy | 363 | TLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKODTIATIIASVVGALFVLVSVL | 422 |

28 243 8.4 398 4 US-09-909-064-84 Sequence 84, Appl
29 243 8.4 398 4 US-09-905-381A-84 Sequence 84, Appl
30 243 8.4 398 4 US-09-906-618-84 Sequence 84, Appl
31 233 8.0 432 4 US-09-778-510-2 Sequence 2, Appl
32 216.5 7.5 4391 4 US-10-006-011A-2 Sequence 2, Appl
33 190.5 6.6 227 4 US-09-205-258-947 Sequence 947, App
34 189.5 6.5 837 4 US-09-949-016-6515 Sequence 6515, Ap
35 187.5 6.5 274 3 US-09-570-367C-19 Sequence 19, Appl
36 187.5 6.5 274 4 US-09-915-524-19 Sequence 19, Appl
37 187.5 6.5 274 4 US-09-934-634-19 Sequence 19, Appl
38 182.5 6.3 819 4 US-09-949-016-11044 Sequence 11044, A
39 173.5 6.0 588 4 US-09-949-016-10547 Sequence 10547, A
40 169 5.8 626 4 US-09-949-016-6213 Sequence 6213, Ap
41 169 5.8 664 4 US-09-949-016-7850 Sequence 7850, Ap
42 167.5 5.8 1709 4 US-09-949-016-10503 Sequence 10503, A
43 166 5.7 1101 3 US-08-986-485-2 Sequence 2, Appl
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45 164 5.7 477 2 US-08-684-594-3 Sequence 3, Appl

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RESULT 2

US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Moryn S.
; APPLICANT: GRAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/201
; CURRENT APPLICATION NUMBER: US/09/723.368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match 22.4%; Score 649.5; DB 4; Length 517;
Best Local Similarity 31.9%; Pred. No. 1e-51;
Matches 167; Conservative 80; Mismatches 182; Indels 95; Gaps 17;
Qy 71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNSMGVSVLAPYRVERFLRPS 103
Qy 128 LNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVPEVPSVLKGPDSLIDG--- 184
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Db 419 PDSDDKKAGPLGG-----SSYEEEEEGGGGERKVGPHPKYDEDAKRPFTVDEAE 475
Qy 506 RPDYDYEDLKMGMKFVSDHYDENEDDLVSHVDGVSISRREWYV 549
Db 476 ARQDGYDRTLGVQY--DPEQLDLAENMVSNQDGSFISKEWYV 517

RESULT 3

US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match 21.6%; Score 627; DB 4; Length 518;
Best Local Similarity 30.8%; Pred. No. 1.3e-49;
Matches 164; Conservative 80; Mismatches 177; Indels 112; Gaps 18;
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Db 215 VPSREAHQOSLACIVNYHM--DRFKESLTLNVQYEPVEVTEGFGNWLQRMVDKLTCKA 272
Qy 294 DANPPPFKS VWSRLDQWPDGLLASNTLHFVHPLTFNYSGVYICKVTSNLSQORSQKVI 353
Db 273 DANPPATEYHWTTLNLSLPKGVQAQRNLTFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
Qy 354 YISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPPFLSTLATIKDPTIATIIASVVGGA 413
Db 333 NITEFPVT---PSPPEHRRAG-----PVP-----TAIGGVAGS 364
Qy 414 LFVLVSVLAGIF-CYRRRTFRGDYFAKNYI-----PPSDMKESQIDV 457
Db 365 ILLVLI-VVGGIIVVALRRRRHTFKGDYSTKKHVYNGYSGAGIPQHHP--MAQNLQ--- 418
Qy 458 LQOEDLSYSDSVSKENK-NPVNNLRKDYLEPEKTOAWN----- 497

Db 419 - YPDDSDDEKKAQPLGG---SSVEEEEEESEGGGGRKVGCPHPKYDEDAKR 467
Qy 498 - VENLNFRPMDYEDLKGKMFVSDHYDENEDDLVSHVDSGVISRRWYV 549
Db 468 PYFTVDEAEARQDGYGRTLGQY--DPEQLDLAENVMSQNDGFSISKWYV 518

RESULT 4
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: High and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 19.58; Score 566; DB 4; Length 458;
Best Local Similarity 31.38; Pred. No. 5.3e-44;
Matches 141; Conservative 75; Mismatches 169; Indels 66; Gaps 12;
Qy 71 GKNSVLKCLIE--VNETTIQISWEKIHGKSSQTVAVHHPGVSQVGEYQGRVLFKNYS 127
Db 44 GTDWLHCSFANPLPSVKITQVTWQKSTNGSKQVAINPSMGVSVLAPYRERVELRPS 103
Qy 128 LNDATITLHNGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIG--- 184
Db 104 FTDGTLRLSLELEDEGVYICGFATFPTGNRESQLNLTWAKPT-NWIEGTQAVLRAKKG 162
Qy 185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLPFTRFARGR 242
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQEIERNPNTVTVISRYRLVPSREAHQ 222
Qy 243 RITCVVKHPALEKDRIYSFILDIOYAEVSVTVGDGNWFGVGRKGVNLKCNADANPPPPFKS 302
Db 223 SLACIVNYHM--DRFKESLINVQYEVIEVIEGPDGNWYLRQMDVKLTCKADANPPATEY 280
Qy 303 VWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRQSKYIISDPPTTT 362
Db 281 HWTTLNGSLPKGVEAQRNLTFFKGPINVSAGTYICEATNPIGTRSGVEVNIKEPR-- 338
Qy 363 TLQPTIOWHSTADIEDLATEPKLPPLSTLTIKDDTTATIIASVVGALFVILVSVL 422
Db 339 -----PQRLG-----SAARLLAGTV--AVFILLVAVL 364
Qy 423 AGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODE-LDSYPPSVKKNKPNVNL 481
Db 365 TVFPLNRQOK-----SPP-----ETDAGTDQPLSQKPEPSRQSSLVPED 407
Qy 482 IRKDYLEPEPEKTQWNNVNLNRRFPRMDIYE 512
Db 408 IQVHL--DPGRQOQOEEEDLQKLSLQPPYD 437

RESULT 5
US-09-949-016-7563
; Sequence 7563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 7563
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7563

Query Match 16.28; Score 469.5; DB 4; Length 522;
Best Local Similarity 26.08; Pred. No. 6.8e-35;
Matches 158; Conservative 78; Mismatches 199; Indels 173; Gaps 23;
Qy 6 RPSGLPC-GGKQAQL-SSASLLGAGLL---QPPTPPPLLLLPLLLFSL-CGALAGP 59
Db 24 RPQSGPRASGRASQPPGPMARAAALLPSRPPTP-----LLWPLLLLLLLETGAQDVR 78
Qy 60 IIVEPHVTAVGMKNVSLKCLII---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQV 115
Db 79 VQVLPEVRGQLGGTVLPCHELLPPVGLYISLVTWQRPDAPANHQNVAAPHKMGPSFPS 138
Qy 116 EYQG--RVLP-----KNYSLNDATITLHNGFSDSGKYICKAVTFPLGNAQSSTT 163
Db 139 PKPGSERLSFSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCFATFPKGSVRGMW 198
Qy 164 VTLLVER-----TVSLIKGPDSDLIDGGNETVAAICIAATGKPVANH-----DWEGDL 210
Db 199 LRVIAPKQNAQAKQVTSQDP-----TTVALCISKEGPPARISWLSLSDWEAKE 249
Qy 211 GEMESTTTSFPNETATIIISQYKLPFTRFARGRITCVVKHHPALEKDIRYSFILDIOYAPE 270
Db 250 TVVSGTLAG---TVVTISRFTLVPSGRADGVTVCKVEHESFEPAALIPVTLVRYPE 305
Qy 271 VSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVWSRLDQWPDGLLASDNTLHFVHPLTF 330
Db 306 VSISGYDDNWLGRDTATLSCDVRNPEPTGYDMSTTSGTFTPTSAVAGSQL-VIHA VDS 364
Qy 331 NYSGVYICKVTNSLQSRQSKYIISDPPTTTTTLQPTIOWHSTADIEDLATEPKLPFP 390
Db 365 LFNFTFVCTVNAVGMGRAEQVIFVRETFR-----PDC----- 394
Qy 391 LSTLATIKDDTTATIIASVVGALFVILVSVLAG-----IFCYRRRTF----- 434
Db 395 ---ASPRD--VGPLWGA VGGTLLVLL--LLAGGSLAFILLRVRRRKSPGGAGGASG 446
Qy 435 -----RGDYFAKNYIPPSDMQKESQIDVLQODELSDYPSVKKNKPNVNL 481
Db 447 DGGFYDPKQAVLGNQDPVFWTVVPVPGPME-----PDG----- 478
Qy 482 IRKDYLEPEPEKTQWNNVNLNRRFPRMDYEDLKGKMFVSDHYDENEDDLVSHVDSGV 541
Db 479 --KDEEEEEE-----EKAEEKGLMLPPPPAL---EDMESQLDGLSL 514
Qy 542 ISRREWYV 549
Db 515 ISRAVTV 522

RESULT 6
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 16.0%; Score 463; DB 4; Length 479;
Best Local Similarity 25.7%; Pred. No. 2.4e-34;
Matches 148; Conservative 76; Mismatches 184; Indels 168; Gaps 20;

Qy 33 PPTPPPLLLLFPPLLFSLR-CGALAGPIIVHPTAVMGKNSLKLI---EVNETITQ 88
Db 13 PPTP-----LLWPLLLLLLLETGAQDVVRVQLPEVRGQLGGTVELPCHLLPPVPLGLYISL 67

Qy 89 ISWEKIHGKSS-QTVAVHHPQYGFVSQGEYQG--RVLF-----KNYSLNDATITL 135
Db 68 VTWQRPDAPAHQNVAAFAHPKMGSPSPKPGSERLSFVSAKOSTGQDTEAELODATAL 127

Qy 136 HNTGFSDSGKIYKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSDLIDGNET 188
Db 128 HGLTVEDEGNTCEFATFPKGSVRGMTWLRVIAPKPKQAEAKVTFSDP-----T 178

Qy 189 VAAICIAATKPKVAHI-----DWEGLGEMESTTTSFPNETATIIISQYKLFPTFRFARGR 242
Db 179 TVALCISKEGRPPARIISWLSLSDWEAKETQVSGTLAG-----TVTVTSRFTLVPSGRADGV 234

Qy 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGNLKNADANPPPPFKS 302
Db 235 TVTCKVEHESFEFEPALIPVTLVRYPEVSIISGDDNWLGRDATALSCDVRNPEPTGY 294

Qy 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSQDKVIYISDPPTTT 362
Db 295 DWSSTTSFTPTSAVAQSQL-VIHAVDSLNTFTVCTVNAVGMRAEQVIFVRETPR-- 351

Qy 363 TLOPTIQMHPSTADIEDLATEPKLPPLSLATIKDDTIATIIASVVGALFVLVSVL 422
Db 352 -----ASPRD--VGPLVMGAVGGTLLVLL--LL 375

Qy 423 AG-----IFCYRRRTF-----RGDYFAKNYIPPSDMQKES 453
Db 376 AGGSLAFILLRVRRRRKSPGGAGGASGDDGFYDPKAQVLNGDPPVFTWTPVPGPME-- 432

Qy 454 QIDVLQODELDSYDPSVKKENPNVNLIRKDYLEBPEKTMNNVENLNFRPMDYYED 513
Db 433 -----PDG-----KDEEEEEEE-----EK 446

Qy 514 LKMGKMFVSDHEHYDENEDDLVSHVDGVSISRREWYV 549

Db 447 AEKGLMLPPPPAL---EDDMESQLDGLSLISRRAVYV 479

RESULT 7

US-09-949-016-6278
; Sequence 6278, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6278
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6278

Query Match 16.0%; Score 463; DB 4; Length 479;
Best Local Similarity 25.7%; Pred. No. 2.4e-34;
Matches 148; Conservative 76; Mismatches 184; Indels 168; Gaps 20;

Qy 33 PPTPPPLLLLFPPLLFSLR-CGALAGPIIVHPTAVMGKNSLKLI---EVNETITQ 88

Db 13 PPTP-----LLWPLLLLLLLETGAQDVVRVQLPEVRGQLGGTVELPCHLLPPVPLGLYISL 67

Qy 89 ISWEKIHGKSS-QTVAVHHPQYGFVSQGEYQG--RVLF-----KNYSLNDATITL 135

Db 68 VTWQRPDAPAHQNVAAFAHPKMGSPSPKPGSERLSFVSAKOSTGQDTEAELODATAL 127

Qy 136 HNTGFSDSGKIYKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSDLIDGNET 188

Db 128 HGLTVEDEGNTCEFATFPKGSVRGMTWLRVIAPKPKQAEAKVTFSDP-----T 178

Qy 189 VAAICIAATKPKVAHI-----DWEGLGEMESTTTSFPNETATIIISQYKLFPTFRFARGR 242

Db 179 TVALCISKEGRPPARIISWLSLSDWEAKETQVSGTLAG-----TVTVTSRFTLVPSGRADGV 234

Qy 243 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGNLKNADANPPPPFKS 302

Db 235 TVTCKVEHESFEFEPALIPVTLVRYPEVSIISGDDNWLGRDATALSCDVRNPEPTGY 294

Qy 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSQDKVIYISDPPTTT 362

Db 295 DWSSTTSFTPTSAVAQSQL-VIHAVDSLNTFTVCTVNAVGMRAEQVIFVRETPR-- 351

Qy 363 TLOPTIQMHPSTADIEDLATEPKLPPLSLATIKDDTIATIIASVVGALFVLVSVL 422

Db 352 -----ASPRD--VGPLVMGAVGGTLLVLL--LL 375

Qy 423 AG-----IFCYRRRTF-----RGDYFAKNYIPPSDMQKES 453

Db 376 AGGSLAFILLRVRRRRKSPGGAGGASGDDGFYDPKAQVLNGDPPVFTWTPVPGPME-- 432

Qy 454 QIDVLQODELDSYDPSVKKENPNVNLIRKDYLEBPEKTMNNVENLNFRPMDYYED 513

Db 433 -----PDG-----KDEEEEEEE-----EK 446

US-09-949-016-6729

Query Match 13.5%; Score 390.5; DB 4; Length 417;
Best Local Similarity 27.6%; Pred. No. 1.1e-27;
Matches 111; Conservative 68; Mismatches 162; Indels 61; Gaps 13;

Qy 44 FPLLLFSLCCAL-----AGPIIVE--PHVTAVMGKNVSLKCLIEVNET----ITQISWEK 93
Db 9 WPLLLVALLVLSWPPPGCTGDVWQAPTQVPGFLGDSVTLFCYLQVPMNEVTHVSQLTWTR 68
Qy 94 IHKSGSOTVAHH---POYGFSGOGEYQGRVLPKNYSLNDATTLHNIIGFSDSGKYICKA 150
Db 69 -HGSESGMAVFHOTQGPSYSESKRLEFVAARL--GAELRNASLMFGLRVEDEGNTCLF 125
Qy 151 VTPPLGNAQSSTTVTLVLEP--TVSLIKGPDLSLIDGNETVAALCIAATGKPVAHIDWEG 208
Db 126 VTFPQGRSVDIMLRVLAKPONTAEVQKVLT----GEPVPMARCVSTGGRPPAQITWHS 181
Qy 209 DLGEMESTT--TGFPNETATIIISQYKLFTRFARGRRITCVVKHPALEKDIRYSFLIDIQ 266
Db 182 DLGMPNTSQVPGFLSGTIVTSLMILVPSQVDGKNTCKVEHSEFEKPLLTVNLTVY 241
Qy 267 YAPEVSVTGDGNWFWGRKGVNLCNADANPPPKSVWSRLDQWPDGLLASDNTLHFVH 326
Db 242 YPPEVSGYDNNWYLCQNEATLTCARSNPETGYNNWSTTMGFLPPFAVQAQQL-LIR 300
Qy 327 PLTFNYSGVVICKVNSLSGORSQKVYISDPPTTTTLQPTIQWHPSTADIEDLATEPKK 386
Db 301 FVDPKPIINTLICNVNALGARQELTVQVKEG----- 333
Qy 387 LPPLSLTLATIKDITATIIASVVGGLFVLVLSVLAGIFYC 428
Db 334 -PSEHSGMSR-----NALIFVLVLGILVFLILGLI--GIFY 366

RESULT 11

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 20

; LENGTH: 442

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-778-510-20

Query Match 11.6%; Score 335.5; DB 4; Length 442;
Best Local Similarity 25.5%; Pred. No. 1.7e-22;
Matches 115; Conservative 87; Mismatches 182; Indels 67; Gaps 18;

Qy 8 SPLCPGGKQALSSASLLGALLLOPTPPPLALLLFPLLLSRLCCALAGPIIVEPHVT 67
Db 3 SVVLPSSGSCAAAAAAPPGLRLR-----LLLLLSA---AALIPGTGQNLFTKQDVT 53
Qy 68 AVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYS 127
Db 54 VIEGEVATISC--QVNSDSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLNFS 103
Qy 128 LNDATITLHNIIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVLEPVTVSIIK-GPDSLIDGNN 186
Db 104 SSELKVSLTNVSIISDEGRYFCQLYTDLP--POESYTTITTVLPPRNLMIDIKQDATIVEG-- 159

Qy 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMESTTTSPNETATIIISQYKLPPTRFAR 240
Db 160 EEIEVNCVTAMASKPATTIRWFKGNTLKGKSEVEEWSDMY-----TVTSQLMKLVHKEDD 214
Qy 241 GRITCVVKHPALEKDIRYSFLIDIOYAPEVSVTGDGNWFWGRKG--VNLKCNADANPP 298
Db 215 GVPVICOVEHPATVGNLQRYLEVQYKPVHIOQMTYPLQGLTREGDALELTCEAIGKPQ 274
Qy 299 PFKSVMSRLDQWPDGCLLASDNTLHFVPLTFNYSGVYICKVNSLSGORSQDKVIYISDP 358
Db 275 PVMVTVRVDDENPQHAVLSGNPL-FINNKNKTNGTYRCEASNIVGKAHSDYMLYVYDP 333
Qy 359 PTTTTLQPTIQWHPSTADIEDLATEPKLPPPLSTLATI-----KDDTIATIIASVVG 411
Db 334 P--TTIPP-----PTTTTTTTTT-----TTTILTIITDSRAGEBSIRAVDHAVIG 378
Qy 412 GALTIVLVSLAGIFCYRRRTFRGDYFAKN 442
Db 379 GVAVVVFAMLCLLI-----ILGRYFARH 402

RESULT 12

US-09-930-803-1

; Sequence 1, Application US/09930803

; Patent No. 6596493

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

; APPLICANT: REEVES, Roger

; APPLICANT: YOSHINORI, Muramaki

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS

; FILE REFERENCE: JHUI770-1

; CURRENT APPLICATION NUMBER: US/09/930,803

; CURRENT FILING DATE: 2001-08-15

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 1

; LENGTH: 442

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-803-1

Query Match 11.6%; Score 335.5; DB 4; Length 442;
Best Local Similarity 25.5%; Pred. No. 1.7e-22;
Matches 115; Conservative 87; Mismatches 182; Indels 67; Gaps 18;

Qy 8 SPLCPGGKQALSSASLLGALLLOPTPPPLALLLFPLLLSRLCCALAGPIIVEPHVT 67
Db 3 SVVLPSSGSCAAAAAAPPGLRLR-----LLLLLSA---AALIPGTGQNLFTKQDVT 53
Qy 68 AVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYS 127
Db 54 VIEGEVATISC--QVNSDSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLNFS 103
Qy 128 LNDATITLHNIIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVLEPVTVSIIK-GPDSLIDGNN 186
Db 104 SSELKVSLTNVSIISDEGRYFCQLYTDLP--POESYTTITTVLPPRNLMIDIKQDATIVEG-- 159
Qy 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMESTTTSPNETATIIISQYKLPPTRFAR 240
Db 160 EEIEVNCVTAMASKPATTIRWFKGNTLKGKSEVEEWSDMY-----TVTSQLMKLVHKEDD 214
Qy 241 GRITCVVKHPALEKDIRYSFLIDIOYAPEVSVTGDGNWFWGRKG--VNLKCNADANPP 298
Db 215 GVPVICOVEHPATVGNLQRYLEVQYKPVHIOQMTYPLQGLTREGDALELTCEAIGKPQ 274
Qy 299 PFKSVMSRLDQWPDGCLLASDNTLHFVPLTFNYSGVYICKVNSLSGORSQDKVIYISDP 358
Db 275 PVMVTVRVDDENPQHAVLSGNPL-FINNKNKTNGTYRCEASNIVGKAHSDYMLYVYDP 333
Qy 359 PTTTTLQPTIQWHPSTADIEDLATEPKLPPPLSTLATI-----KDDTIATIIASVVG 411
Db 334 P--TTIPP-----PTTTTTTTTT-----TTTILTIITDSRAGEBSIRAVDHAVIG 378

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QY      412  GALFIVLVSVLAGIFCYRRRTFRGDYFAKN  442
      | : | : | : | : | : | : | : | : | : | :
Db      379  GVVAVVVFAMLCLLI-----ILGRYFARH  402

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RESULT 13
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bosteijn, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William

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| | | | | | | | | | |
|-----------------------|--------|--|----------|------------|------|--------|------|------|-----|
| Query Match | 11.5%; | Score | 333.5; | DB | 4; | Length | 440; | | |
| Best local Similarity | 25.7%; | Pred. No. | 2.6e-22; | | | | | | |
| Matches | 117; | Conservative | 85; | Mismatches | 176; | Indels | 77; | Gaps | 20; |
| QY | 8 | SPLCPGGGKAQLSSASILGAGLLQLPPTPPPLLLLPFLLLLSRLCAGALA---- <td>63</td> | 63 | | | | | | |
| DB | 3 | SVVLPSGSQCAAAAA-----RAPGRLRL-----LLIFS--AAALPTGGQQLMFT | 47 | | | | | | |
| QY | 64 | PHYTAWGNKNSVLCCLIEVNETITQIGWEKIHGKSQTVAHHPOYGSVQGEYQGRVLF | 123 | | | | | | |
| DB | 48 | KDVTVEIGEVAATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFPLKDSRFQL | 97 | | | | | | |
| QY | 124 | KNYSLNDAITILNIGFSDSGKYICKAVTAPPLGNAQSSITTVULVETVSLIK--GPDSLI | 182 | | | | | | |
| DB | 98 | LNFSSSSLKSLVSNVSISSDEGRYFCQLYTDP--PQESYTTITVLVPPNLMIDIQKDTAV | 155 | | | | | | |
| QY | 183 | DGNGNETVAACIAATGKPVAHIDW--EGDL-----GEMESTTSPFNATATISQYKLPPT | 236 | | | | | | |
| DB | 156 | EG--EEEVNCTAMASAPATIRWFKGNTLKGKSEVEWSDMY-----TVTSQMLKVH | 208 | | | | | | |
| QY | 237 | RPARGRITCVKHPALEKDIRYSFIIDIQYAPEVSVTGYDGNWFWGKRG--VNLKCNAD | 294 | | | | | | |
| DB | 209 | KEDDGVPMVCQVEHPAVTGNLQRYLYEVQYKPVQHIQMTVPLQGLTREGDALELTCEAI | 268 | | | | | | |
| QY | 295 | ANPPPPKSVNSRLDQWPDGGLASDNLHFVHPLTFNYSGVYICKVNSLQGRSDQKVIY | 354 | | | | | | |
| DB | 269 | GKQPVMVTWVRVDENPQHAVLSGPNL--FINNLKTDNGTYRCEASNIVGKASHDYMLY | 327 | | | | | | |
| QY | 355 | ISDPPTTTTTLQPTTIQWHPSTADIEDLATEPKKLPPLSLTATI-----KDDTIATIIA | 407 | | | | | | |
| DB | 328 | VYDPP--TTTTP-----PTTTTTTTTTT-----TTTILITDSRAGEEGSIRAVDH | 372 | | | | | | |
| QY | 408 | SVVGGALFIVLVSVLAGIFCYRRRRTRFRGDYFAXN | 442 | | | | | | |

Db 373 AVIGGVAVVVFAMCLLI-----ILGRYFARH 400

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RESULT 14
US/09-944-457-61
; Sequence 61, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kijavin,Ivay
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRAN
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,082
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,236
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998

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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 255.269 Seconds
(without alignments)
894.712 Million cell updates/sec

Title: US-09-972-268-6
Perfect score: 2901
Sequence: 1 MARTLRPSPLCPGGKAQLS.....EDDLVSHVDSVISRREWYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|--------|--------------|-------|--|
| 1 | 2901 | 100.0 | 549 | 10 US-09-972-268-6 Sequence 6, Appli |
| 2 | 2901 | 100.0 | 549 | 14 US-10-161-572-45 Sequence 45, Appli |
| 3 | 2887 | 99.5 | 549 | 10 US-09-972-268-4 Sequence 4, Appli |
| 4 | 2866 | 98.8 | 542 | 10 US-09-972-268-2 Sequence 2, Appli |
| 5 | 2721 | 93.8 | 549 | 10 US-09-959-845-2 Sequence 2, Appli |
| 6 | 2721 | 93.8 | 549 | 10 US-09-972-268-17 Sequence 17, Appli |
| 7 | 2120 | 73.1 | 426 | 10 US-09-972-268-15 Sequence 15, Appli |
| 8 | 2120 | 73.1 | 634 | 10 US-09-972-268-13 Sequence 13, Appli |
| 9 | 1920.5 | 66.2 | 510 | 10 US-09-972-268-12 Sequence 12, Appli |
| 10 | 1906.5 | 65.7 | 510 | 10 US-09-972-268-10 Sequence 10, Appli |
| 11 | 1902.5 | 65.6 | 437 | 10 US-09-972-268-31 Sequence 31, Appli |

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| 12 | 1892.5 | 65.2 | 504 | 10 US-09-972-268-8 Sequence 8, Appli |
| 13 | 1889 | 65.1 | 595 | 10 US-09-972-268-14 Sequence 14, Appli |
| 14 | 1878 | 64.7 | 387 | 10 US-09-972-268-16 Sequence 16, Appli |
| 15 | 1814.5 | 62.5 | 510 | 10 US-09-959-845-4 Sequence 4, Appli |
| 16 | 1814.5 | 62.5 | 510 | 10 US-09-972-268-18 Sequence 18, Appli |
| 17 | 1809.5 | 62.4 | 438 | 10 US-09-959-845-6 Sequence 6, Appli |
| 18 | 1809.5 | 62.4 | 438 | 10 US-09-972-268-19 Sequence 19, Appli |
| 19 | 1355 | 46.7 | 258 | 15 US-10-264-237-2626 Sequence 2626, Ap |
| 20 | 649.5 | 22.4 | 514 | 14 US-10-161-572-60 Sequence 60, Appli |
| 21 | 649.5 | 22.4 | 517 | 10 US-09-972-268-20 Sequence 20, Appli |
| 22 | 627 | 21.6 | 518 | 9 US-09-919-172-20 Sequence 20, Appli |
| 23 | 627 | 21.6 | 518 | 16 US-10-752-986-20 Sequence 20, Appli |
| 24 | 569 | 19.6 | 458 | 10 US-09-972-268-21 Sequence 21, Appli |
| 25 | 548 | 18.9 | 510 | 15 US-10-422-571-5 Sequence 5, Appli |
| 26 | 544 | 18.9 | 510 | 15 US-10-422-571-31 Sequence 31, Appli |
| 27 | 544 | 18.8 | 510 | 10 US-09-766-511B-33 Sequence 33, Appli |
| 28 | 544 | 18.8 | 510 | 14 US-10-241-220-94 Sequence 94, Appli |
| 29 | 544 | 18.8 | 510 | 15 US-10-295-027-66 Sequence 66, Appli |
| 30 | 544 | 18.8 | 510 | 15 US-10-173-999-76 Sequence 76, Appli |
| 31 | 544 | 18.8 | 510 | 15 US-10-058-270A-54 Sequence 54, Appli |
| 32 | 544 | 18.8 | 510 | 15 US-10-188-832-179 Sequence 179, App |
| 33 | 544 | 18.8 | 510 | 15 US-10-422-571-3 Sequence 3, Appli |
| 34 | 544 | 18.8 | 510 | 15 US-10-422-571-7 Sequence 7, Appli |
| 35 | 544 | 18.8 | 510 | 15 US-10-422-571-9 Sequence 9, Appli |
| 36 | 544 | 18.8 | 510 | 15 US-10-422-571-11 Sequence 11, Appli |
| 37 | 544 | 18.8 | 510 | 15 US-10-422-571-17 Sequence 17, Appli |
| 38 | 544 | 18.8 | 510 | 15 US-10-422-571-25 Sequence 25, Appli |
| 39 | 544 | 18.8 | 510 | 15 US-10-422-571-30 Sequence 30, Appli |
| 40 | 544 | 18.8 | 510 | 15 US-10-422-571-36 Sequence 36, Appli |
| 41 | 544 | 18.8 | 510 | 15 US-10-422-571-40 Sequence 40, Appli |
| 42 | 544 | 18.8 | 510 | 15 US-10-422-571-41 Sequence 41, Appli |
| 43 | 544 | 18.8 | 510 | 15 US-10-422-571-42 Sequence 42, Appli |
| 44 | 544 | 18.8 | 510 | 15 US-10-422-571-82 Sequence 82, Appli |
| 45 | 544 | 18.8 | 510 | 15 US-10-422-571-115 Sequence 115, App |

ALIGNMENTS

RESULT 1

US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TI
; FILE REFERENCE: 3101-A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

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| Query Match | 100.0%; | Score 2901; | DB 10; | Length 549; |
| Best Local Similarity | 100.0%; | Pred. No. 1.5e-214; | | |
| Matches 549; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | MARTLRPSPLCPGGKAQLSSALIGLGLLQPTPPPLLLLPPLLLFSLRCGALAGPI | 60 | |
| Db | 1 | MARTLRPSPLCPGGKAQLSSALIGLGLLQPTPPPLLLLPPLLLFSLRCGALAGPI | 60 | |
| Qy | 61 | IVPHTVAVGKGVSLKCLIEVNETITQISWEKHGKSQTVAVHHPOYGFSGVQGR | 120 | |

Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
Db 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTRFAR 240
QY 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGDGNMFVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGDGNMFVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDQWPGDGLASDNTLHFVHPLTFNYSVGVIKVTNSLQORSQDKVIYISDPPT 360
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QY 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSLTLATIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKENKPNVNN 480
Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKENKPNVNN 480
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Db 481 LIRKDYLEPEKTOQNNVENLNRFERPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 2

US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 100.0%; Score 2901; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.5e-214;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDS 180
QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTRFAR 240
QY 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGDGNMFVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVKHPALEKDIRYSFILDIOYAPEVSVTGDGNMFVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDQWPGDGLASDNTLHFVHPLTFNYSVGVIKVTNSLQORSQDKVIYISDPPT 360
Db 301 KSVWSRLDQWPGDGLASDNTLHFVHPLTFNYSVGVIKVTNSLQORSQDKVIYISDPPT 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSLTLATIKDDTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPLSLTLATIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKENKPNVNN 480
Db 421 VLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELDSYDPSVKENKPNVNN 480
QY 481 LIRKDYLEPEKTOQNNVENLNRFERPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVENLNRFERPMDYEDLKMGMKFSVDEHYDENEDDLVSHVDGS 540
QY 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 3

US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 99.5%; Score 2887; DB 10; Length 549;
Best Local Similarity 99.6%; Pred. No. 1.8e-213;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVKHPALSKDIRYSFILDIOVAPEVSVTGYDGNWFGKGNLKNADANPPPF 300
Db 241 GRRITCVKHPALSKDIRYSFILDIOVAPEVSVTGYDGNWFGKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVISDPT 360
Db 301 KSVMSRLDGQPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVISDPT 360
Qy 361 TTTLOPTQIOWHPSTADIEDLATEPKLPFPLSTLTIATIKDDTIATIIASVVGALFIVLS 420
Db 361 TTTLOPTQIOWHPSTADIEDLATEPKLPFPLSTLTIATIKDDTIATIIASVVGALFIVLS 420
Qy 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPVNN 480
Db 421 VLAGIFCYRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPVNN 480
Qy 481 LIRKDYLEPEKTOQNNVNNLNRPERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVNNLNRPERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGS 540
Qy 541 VISRREWV 549
Db 541 VISRREWV 549

RESULT 4

US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 98.8%; Score 2866; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 7.2e-212; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0;

Qy 8 SPLCPGGGKAQLSSASLIGALLQPTPPPLLLLPFLLSLCCGALGPIIVEPHVT 67
Db 1 SPLCPGGGKAQLSSASLIGALLQPTPPPLLLLPFLLSLCCGALGPIIVEPHVT 60
Qy 68 AVWGNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQGYQGRVLFKNYS 127
Db 61 AVWGNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQGYQGRVLFKNYS 120
Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVEPTVSLIKGPD 187
Db 121 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVEPTVSLIKGPD 180

Qy 188 TVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTRFARQRRITCV 247
Db 181 TVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTRFARQRRITCV 240
Qy 248 VKHPALSKDIRYSFILDIOVAPEVSVTGYDGNWFGKGNLKNADANPPPFKSVMSRL 307
Db 241 VKHPALSKDIRYSFILDIOVAPEVSVTGYDGNWFGKGNLKNADANPPPFKSVMSRL 300
Qy 308 DGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVISDPTTTTLOPT 367
Db 301 DGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVISDPTTTTLOPT 360
Qy 368 IQWHPSTADIEDLATEPKLPFPLSTLTIATIKDDTIATIIASVVGALFIVLSVLGIFC 427
Db 361 IQWHPSTADIEDLATEPKLPFPLSTLTIATIKDDTIATIIASVVGALFIVLSVLGIFC 420
Qy 428 YRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPVNNLIRKDY 487
Db 421 YRRRTFRGDFYFAKNYIPPSDMQKESQIDVLQDDELSDYPSVKENKNPVNNLIRKDY 480
Qy 488 EEPKTOQNNVNNLNRPERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGSVISRREW 547
Db 481 EEPKTOQNNVNNLNRPERPMDYEDLKMGMKFVSDHYDENEDDLVSHVDGSVISRREW 540
Qy 548 YV 549
Db 541 YV 542

RESULT 5

US-09-959-845-2
; Sequence 2, Application US/09959845
; Publication No. US2003008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-2

Query Match 93.8%; Score 2721; DB 10; Length 549;
Best Local Similarity 92.9%; Pred. No. 1.1e-200;
Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MARTLRSPICPGGKAQLSSASLIGALLQPTPPPLLLLPFLLSLCCGALGPI 60
Db 1 MARTLRSPICPGGKAQLSSASLIGALLQPTPPPLLLLPFLLSLCCGALGPI 60
Qy 61 IVPHVTAVWGNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQGYQGR 120
Db 61 IVPHVTAVWGNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFSGVQGYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTRFAR 240

```
Db 181 LIDGNETVAACVAATGKFPVQIADWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
Qy 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISDPPT 360
Db 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISDPPT 360
Qy 361 TTTLQPTQIOWHPSTADIEDLATPEPKLPPLSTLATIKDDTIATIIASVVGALFVLVLS 420
Db 361 TTTLQPTQVQWSSPADVDIATEHKKLPPLSTLATIKDDTIATIIASVVGALFVLVLS 420
Qy 421 VLAGIFCYRRRTFRGDYFAKNYIPSDMQKESQIDVLQODELDSYDPSVKKENKNPVNN 480
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPSDMQKESQIDVLHODELDSYDPSVKKENKNPVNN 480
Qy 481 LIRKDYLEPEKTOQNNVENLNRFRPMDYYEDLKMGKMFVSDERHEDDVLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVENLNRFRPMDYYEDLKMGKMFVSDERHEDDVLVSHVDGS 540
Qy 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 6
US-09-972-268-17
; Sequence 17, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-17

Query Match 93.8%; Score 2721; DB 10; Length 549;
Best Local Similarity 92.9%; Pred. No. 1.1e-200;
Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MARTLRSPCLPCGGKAQLSSALLGALLLOPPTPPPLLLLPPLLLFSLRCGALAGPI 60
Db 1 MARTPGAPLPCGGKAQLSSAFPAPAGLLLPAPTTPPLLLLPPLLLFSLRCGALAGSI 60
Qy 61 IVEPHVTAVWGKVNLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Db 61 IVEPHVTAVWGKVNLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVHAIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
Db 181 LIDGNETVAACVAATGKFPVQIADWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
Qy 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
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Db 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISDPPT 360
Db 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISDPPT 360
Qy 361 TTTLQPTQIOWHPSTADIEDLATPEPKLPPLSTLATIKDDTIATIIASVVGALFVLVLS 420
Db 361 TTTLQPTQVQWSSPADVDIATEHKKLPPLSTLATIKDDTIATIIASVVGALFVLVLS 420
Qy 421 VLAGIFCYRRRTFRGDYFAKNYIPSDMQKESQIDVLQODELDSYDPSVKKENKNPVNN 480
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPSDMQKESQIDVLHODELDSYDPSVKKENKNPVNN 480
Qy 481 LIRKDYLEPEKTOQNNVENLNRFRPMDYYEDLKMGKMFVSDERHEDDVLVSHVDGS 540
Db 481 LIRKDYLEPEKTOQNNVENLNRFRPMDYYEDLKMGKMFVSDERHEDDVLVSHVDGS 540
Qy 541 VISRREWYV 549
Db 541 VISRREWYV 549

RESULT 7
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match 73.1%; Score 2120; DB 10; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.5e-154;
Matches 402; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTLRSPCLPCGGKAQLSSALLGALLLOPPTPPPLLLLPPLLLFSLRCGALAGPI 60
Db 1 MARTPGAPLPCGGKAQLSSALLGALLLOPPTPPPLLLLPPLLLFSLRCGALAGPI 60
Qy 61 IVEPHVTAVWGKVNLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Db 61 IVEPHVTAVWGKVNLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVHAIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
Db 181 LIDGNETVAACIAATGKPVHAIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
Qy 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRITCVVWHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
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Qy 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPT 360
Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPT 360
Qy 361 TTTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIAT 404
Db 361 TTTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIAT 404

RESULT 8

US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 73.1%; Score 2120; DB 10; Length 634;
Best Local Similarity 99.5%; Pred. No. 2.6e-154;
Matches 402; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTLRSPCLPGGKAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
Db 1 MARTPGSPCLPGGKAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICAAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAAICAAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPT 360
Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPT 360
Qy 361 TTTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIAT 404
Db 361 TTTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIAT 404

RESULT 9

US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match 66.2%; Score 1920.5; DB 10; Length 510;
Best Local Similarity 67.9%; Pred. No. 4.4e-139;
Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
Qy 1 MARTLRSPCLPGGKAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
Db 1 MARTLRSPCLPGGKAQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICAAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAAICAAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPT 360
Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPT 360
Qy 361 TTTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGALFIVLS 420
Db 360 -----FKQTSSIAVAGAVIGAVLALFIIA 383
Qy 421 VLAGIFCYRRRRTRFGDYFAKNY-IPPSDMQKESQIDVLOQDELDSDYPSYKKNKPNV- 478
Db 384 IFVTVLTPRKK-RPSYLDKVIDLPETHK-----PPPLYEERSPLP 424
Qy 479 -NNLIRKDYLEEBKTKQW-----NNVENLRF-ERPMDYVEDLKQMKFVSD----- 523
Db 425 QKDLFQPEHL--PLQTFKEREVGNLQHSNGLNRSRFDYEDENPVGEDIQOMPLYNQM 482
Qy 524 -----EHYDENEDDLVSHVDGSVLSRREYV 549
Db 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510

RESULT 10

US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.

```
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match      65.7%; Score 1906.5; DB 10; Length 510;
Best Local Similarity 67.6%; Pred. No. 5.3e-138;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;

QY 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFRLCGALAGPI 60
Db 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFRLCGALAGPI 60
QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFVSQGEYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNATATIIISQYKLFPTRFAR 240
Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNATATIIISQYKLFPTRFAR 240
QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDQWPDGLASNTLHFVHPLTFNYSGVVICKVTNSLGORSQDKVIYISDVP 360
Db 301 KSVMSRLDQWPDGLASNTLHFVHPLTFNYSGVVICKVTNSLGORSQDKVIYISDVP 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDPTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDPTIATIIASVVGALFVLVS 420
QY 421 VLAGICYRRRTFRGDYFAKNY-IPPSDMQKSQIDVLQOQDELSDYPSVSKENKNPV- 478
Db 421 VLAGICYRRRTFRGDYFAKNY-IPPSDMQKSQIDVLQOQDELSDYPSVSKENKNPV- 478
QY 479 -NNLIRKDYEEPEKQW-----NNVENLNR-ERPMDYVEDLKMGMKFVSD----- 523
Db 479 -NNLIRKDYEEPEKQW-----NNVENLNR-ERPMDYVEDLKMGMKFVSD----- 523
QY 425 QKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGDGIGQVMVPLYNQM 482
Db 425 QKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGDGIGQVMVPLYNQM 482
QY 524 -----EHDNEDDLVSHVDGVSISRREWY 549
Db 524 -----EHDNEDDLVSHVDGVSISRREWY 549
QY 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
Db 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510

RESULT 11
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
```

```
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match      65.6%; Score 1902.5; DB 10; Length 437;
Best Local Similarity 79.3%; Pred. No. 8.6e-138;
Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFRLCGALAGPI 60
Db 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFRLCGALAGPI 60
QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFVSQGEYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNATATIIISQYKLFPTRFAR 240
Db 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNATATIIISQYKLFPTRFAR 240
QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDQWPDGLASNTLHFVHPLTFNYSGVVICKVTNSLGORSQDKVIYISDVP 360
Db 301 KSVMSRLDQWPDGLASNTLHFVHPLTFNYSGVVICKVTNSLGORSQDKVIYISDVP 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDPTIATIIASVVGALFVLVS 420
Db 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDPTIATIIASVVGALFVLVS 420
QY 421 VLAGICYRRRTFRGDYFAK-----NYIPPSDMQKES-----QIDVLQ 459
Db 421 VLAGICYRRRTFRGDYFAK-----NYIPPSDMQKES-----QIDVLQ 459
QY 384 IFVTLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430
Db 384 IFVTLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430

RESULT 12
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
```

US-09-972-268-8

Query Match 65.2%; Score 1892.5; DB 10; Length 504;
Best Local Similarity 67.6%; Pred. No. 6.2e-137;
Matches 384; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

Qy 7 PSLPCPGGGAQSLSSASLLGAGLLQLQPTTPTTLLPPLLLFRLCGALAGPIIIVPHV 66
Db 1 PSLPCPGGGAQSLSSASLLGAGLLQLQPTTPTTLLPPLLLFRLCGALAGPIIIVPHV 60
Qy 67 TAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSVQGEYQGRVLFKNY 126
Db 61 TAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSVQGEYQGRVLFKNY 120
Qy 127 SLNDATITLHNGFSDSGKYICKAVTTPPLGNAQSSTTTTLVVEPTVSLIKGPDLSLDGNN 186
Db 121 SLNDATITLHNGFSDSGKYICKAVTTPPLGNAQSSTTTTLVVEPTVSLIKGPDLSLDGNN 180
Qy 187 ETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATTISQYKLPFTRFARGRITC 246
Db 181 ETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATTISQYKLPFTRFARGRITC 240
Qy 247 VVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPKSVWSR 306
Db 241 VVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPKSVWSR 300
Qy 307 LDGOWPDGLLASDNTLHFVHPLTFNYSVGIKVTNSLGQRSDQKVIYISDPPTTLTLP 366
Db 301 LDGOWPDGLLASDNTLHFVHPLTFNYSVGIKVTNSLGQRSDQKVIYISDPPTTLTLP 360
Qy 367 TIQWHPSTADIEDLATEPKLPPLSLTATIKDTIATIIASVVGALFVLVSLVLAGIF 426
Db 354 TIQWHPSTADIEDLATEPKLPPLSLTATIKDTIATIIASVVGALFVLVSLVLAGIF 420
Qy 427 CYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQDDELSDYPSVKKENKNPV--NNLVR 483
Db 384 LTPKCK--RSYLDKVIDLPPTHK-----PPPLYEERSPPLPQKDLFQ 424
Qy 484 KQYLEPEKTKQW-----NNVENLNR-ERPMDYVEDLKMGMKFVSD----- 523
Db 425 PEHL--PLQTFKEREVGNLQHSNLSRFDYEDENPVGEDGIGQWPLYNQMCYQDRS 482
Qy 524 --EHYDENEDDLYSHVDGVSISRREWYV 549
Db 483 PGKHQNNDPKRV-----YIDPREHYV 504

RESULT 13

US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Farnlow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match

Best Local Similarity 76.0%; Score 1889; DB 10; Length 595;
Matches 381; Conservative 16; Mismatches 72; Indels 32; Gaps 5;

Qy 1 MARTLRPSPLCPGCGKAQSLSSASLLGAGLLQLQPTTPTTLLPPLLLFRLCGALAGPI 60
Db 1 MARTLRPSPLCPGCGKAQSLSSASLLGAGLLQLQPTTPTTLLPPLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSVQGEYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSVQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNGFSDSGKYICKAVTTPPLGNAQSSTTTTLVVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNGFSDSGKYICKAVTTPPLGNAQSSTTTTLVVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATTISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATTISQYKLPFTRFAR 240
Qy 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSVGIKVTNSLGQRSDQKVIYISDPPT 360
Db 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSVGIKVTNSLGQRSDQKVIYISDPPT 360
Qy 361 TTTTLQ-----PTIQWHPSTADIEDLATEPKLPPLSLTATIKDTIATII 406
Db 361 KQTSRRSCDTHTCPPCPAPEAGPSV-----FLFPK-----PKDILMSRTEVTCVV 411
Qy 407 ASVVGALFVLVSLVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELSDY 466
Db 412 VDVSHEDPEVKFNWYVDGVEVHNAKTPREQVNSTY-----RVSVSLTVLHQDWLNGK 465
Qy 467 PDSVKKENK---NPVNNLIRK 484
Db 466 EYCKVSNKALPAPIETKISK 486

RESULT 14

US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Farnlow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match

Best Local Similarity 98.3%; Score 1878; DB 10; Length 387;
Matches 357; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGCGKAQSLSSASLLGAGLLQLQPTTPTTLLPPLLLFRLCGALAGPI 60
Db 1 MARTLRPSPLCPGCGKAQSLSSASLLGAGLLQLQPTTPTTLLPPLLLFRLCGALAGPI 60

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Db 1 MARTPGSPPLCPGGKAQLSSALLGAGLLQLQPTPPPLLLLPPLLLFSRLCGALAGPI 60
QY 1 IVEPHVTAVWGKNSVKCLIEVNETTQISWEKIHGKSSQTVAVHHPQYGFSGVQGYQGR 120
Db 61 IVEPHVTAVWGKNSVKCLIEVNETTQISWEKIHGKSSQTVAVHHPQYGFSGVQGYQGR 120
QY 121 VLFKNYSLNDATTILHNI GFSDSGKYICKAVTFLGNAQSSTTVTLVVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTILHNI GFSDSGKYICKAVTFLGNAQSSTTVTLVVEPTVSLIKGPD 180
QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
QY 241 GRRITCVVHPALEKDIRYSFILDIOYAPBVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOYAPBVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVYIISDPPT 360
Db 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVYIISDPPT 360
QY 361 TTT 363
Db 361 KQT 363

RESULT 15
US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4

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Query Match 62.5%; Score 1814.5; DB 10; Length 510;
 Best Local Similarity 66.4%; Pred. No. 6.4e-131;
 Matches 374; Conservative 39; Mismatches 83; Indels 67; Gaps 10;

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QY 1 MARTLRSPLCPGGKAQLSSALLGAGLLQLQPTPPPLLLLPPLLLFSRLCGALAGPI 60
Db 1 MARTPGAPLCPGGKAQLSSAPPAAGLLLPAPTPPPPLLLLPPLLLFSRLCGALAGSI 60
QY 61 IVEPHVTAVWGKNSVKCLIEVNETTQISWEKIHGKSSQTVAVHHPQYGFSGVQGYQGR 120
Db 61 IVEPHVTAVWGKNSVKCLIEVNETTQISWEKIHGKSTQTVAVHHPQYGFSGVQGYQGR 120
QY 121 VLFKNYSLNDATTILHNI GFSDSGKYICKAVTFLGNAQSSTTVTLVVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTILHNI GFSDSGKYICKAVTFLGNAQSSTTVTLVVEPTVSLIKGPD 180
QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFAR 240
QY 241 GRRITCVVHPALEKDIRYSFILDIOYAPBVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300

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Db 241 GRRITCVVHPALEKDIRYSFILDIOYAPBVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVYIISDPPT 360
Db 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVYIISDPPT 360
QY 361 TTTLQPTIQMHPSTADIEDLATEPKKLPPLSLTLATIKODTIIATIASVVGGALFVLVS 420
Db 361 TQT-----SSIA-----VAGAVIGAVLALFIIT 383
QY 421 VLAGIPCYRRRTFRGDFYFAKNY-IPPSDMQK---ESQIDVLQOQDEL----DSYPSVSKK 472
Db 384 VFTVLLTTRKK--RPSYLDKVIDLPPTHKPPPVVEERIPSLPQKDLGQTEHLPLQTOF 441
QY 473 ENK-----NPVNNLIRKOYLEBEPEKT-QMNNVENLNRPERPMDYEDLKMGMKFVSDHY 526
Db 442 KEKGAGGLQPSNGPISRRRPFDEDESTMQBDGTQRMCPLYSQMCHQDRSPR-----QHH 494
QY 527 DENEDDLVSHVDGSGVTSRREWYV 549
Db 495 PRNPERL-----YINPREHYV 510

```

Search completed: October 6, 2005, 09:33:43
 Job time : 257.269 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 84.2348 Seconds
(without alignments)
2341.642 Million cell updates/sec

Title: US-09-972-268-10
Perfect score: 2711
Sequence: 1 MARTPGSPCLPGGKQAQLS.....KHQNDPKRVYIDPREHYV 510

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 2711 | 100.0 | 510 | 5 | Aae23285 Mouse nec |
| 2 | 2693 | 99.3 | 510 | 5 | Aae23286 Human nec |
| 3 | 2679 | 98.8 | 504 | 5 | Aae23284 Human del |
| 4 | 2406 | 88.7 | 510 | 4 | Aag63983 Amino aci |
| 5 | 2406 | 88.7 | 510 | 5 | Aae23292 Mouse nec |
| 6 | 2243 | 82.7 | 437 | 5 | Aae23299 Human nec |
| 7 | 2125 | 78.4 | 438 | 4 | Aag63984 Amino aci |
| 8 | 2125 | 78.4 | 438 | 5 | Aae23293 Mouse nec |
| 9 | 1932 | 71.3 | 595 | 5 | Aae23288 Human nec |
| 10 | 1930 | 71.2 | 387 | 5 | Aae23290 Human nec |
| 11 | 1924.5 | 71.0 | 549 | 5 | Aae23282 Mouse nec |
| 12 | 1906.5 | 70.3 | 549 | 5 | Aae23283 Human nec |
| 13 | 1906.5 | 70.3 | 549 | 6 | ABJ20222 Human IG |
| 14 | 1906.5 | 70.3 | 549 | 8 | ADR66369 Human pro |
| 15 | 1906.5 | 70.3 | 549 | 8 | ADR66711 Human pro |
| 16 | 1903.5 | 70.2 | 634 | 5 | Aae23287 Human nec |
| 17 | 1898 | 70.0 | 426 | 5 | Aae23289 Human nec |
| 18 | 1885.5 | 69.5 | 542 | 5 | Aae23281 Human del |
| 19 | 1883.5 | 69.5 | 555 | 4 | AAM39143 Human pol |
| 20 | 1837.5 | 67.8 | 549 | 4 | Aag63982 Amino aci |
| 21 | 1837.5 | 67.8 | 549 | 4 | Aag63985 Amino aci |
| 22 | 1837.5 | 67.8 | 549 | 5 | Aae23291 Mouse nec |
| 23 | 1794 | 66.2 | 559 | 4 | AAM40929 Human pol |
| 24 | 1235 | 45.6 | 267 | 4 | AAM93536 Human pol |
| 25 | 1235 | 45.6 | 267 | 8 | ADL31248 Human pro |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 26 | 642.5 | 23.7 | 305 | 5 | ADR41425 | Adr41425 Human CD- |
| 27 | 588 | 21.7 | 514 | 6 | ABJ20237 | ABJ20237 Human IG |
| 28 | 588 | 21.7 | 517 | 3 | AAJ23290 | Aaj23290 Herpesvir |
| 29 | 588 | 21.7 | 517 | 5 | AAE23294 | Aae23294 Human nec |
| 30 | 587.5 | 21.7 | 458 | 5 | AAE23295 | Aae23295 Human nec |
| 31 | 565.5 | 20.9 | 518 | 5 | ABG77170 | Abg77170 Prostata |
| 32 | 551.5 | 20.3 | 578 | 8 | ADP03592 | Adp03592 Infection |
| 33 | 543 | 20.0 | 580 | 8 | ADO47877 | Ado47877 Alpha-Her |
| 34 | 543 | 20.0 | 581 | 8 | ADP03590 | Adp03590 Infection |
| 35 | 540 | 19.9 | 530 | 8 | ADJ76222 | Adj76222 Marker ge |
| 36 | 538.5 | 19.9 | 485 | 8 | ADK83283 | Adk83283 Human 191 |
| 37 | 538.5 | 19.9 | 485 | 8 | ADK83298 | Adk83298 Human 191 |
| 38 | 538.5 | 19.9 | 485 | 8 | ADK83184 | Adk83184 Human 191 |
| 39 | 538.5 | 19.9 | 485 | 8 | ADK83202 | Adk83202 Human 191 |
| 40 | 538.5 | 19.9 | 485 | 8 | ADK83285 | Adk83285 Human 191 |
| 41 | 538.5 | 19.9 | 497 | 5 | AAE23303 | Aae23303 Human nec |
| 42 | 537 | 19.8 | 498 | 5 | AAE23305 | Aae23305 Human nec |
| 43 | 530.5 | 19.6 | 352 | 8 | ABM83397 | Abm83397 Human dia |
| 44 | 530.5 | 19.6 | 353 | 8 | ABM83396 | Abm83396 Human dia |
| 45 | 530.5 | 19.6 | 353 | 8 | ABM83395 | Abm83395 Human dia |

ALIGNMENTS

RESULT 1
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX AC AAE23285;
XX DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX DB Mouse nectin-3-human nectin-3beta fusion protein.
XX KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX FH Key Location/Qualifiers
FT Region 1..6
FT Region /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT Region /note= "Human nectin-3beta protein"
XX WO200228902-A2.
XX PD 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US031392.
XX PR 05-OCT-2000; 2000US-0238557P.
XX FA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI: 2002-426103/45.
XX N-PSDB; AAD37444.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX Claim 1; Page 94-95; 141pp; English.
PS

```

XX CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 510 AA;

Query Match 100.0%; Score 2711; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 7.1e-217; Indels 0; Gaps 0;
Matches 510; Conservative 0; Mismatches 0;

Qy 1 MARTPGSPPLCPGGKQALSSASLLGAGLLQLPPTPPPLLLLPPLLLFRLCGALAGPI 60
Db 1 MARTPGSPPLCPGGKQALSSASLLGAGLLQLPPTPPPLLLLPPLLLFRLCGALAGPI 60

Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSGEYQGR 120
Db 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSGEYQGR 120

Qy 121 VLFKNYSINDATITLHNIGSDSKYICKAVTFPLGNAQSGSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGSDSKYICKAVTFPLGNAQSGSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFNETATIIISQYKLPPTRFAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFNETATIIISQYKLPPTRFAR 240

Qy 241 GRRITCVVXHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGNLKNADANPPFF 300
Db 241 GRRITCVVXHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGNLKNADANPPFF 300

Qy 301 KSVMSRLDGQWPDGILLASDNTLHFVHPLTENYSGVYICKVTNSLGORSQDKVIYISDVPF 360
Db 301 KSVMSRLDGQWPDGILLASDNTLHFVHPLTENYSGVYICKVTNSLGORSQDKVIYISDVPF 360

Qy 361 KQTSIAVAGAVIGALVLFIAIFVTVLLTPPKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KQTSIAVAGAVIGALVLFIAIFVTVLLTPPKRPSYLDKVIDLPPTHKPPPLYEERS 420

Qy 421 PPLPKQLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSFDYEDENPNVGEDGIQMYPLYN 480
Db 421 PPLPKQLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSFDYEDENPNVGEDGIQMYPLYN 480

Qy 481 QMCYQDRSPGKHQNDPKRVIIDPREHYV 510
Db 481 QMCYQDRSPGKHQNDPKRVIIDPREHYV 510

RESULT 2
AAE23286
ID AAE23286 standard; protein; 510 AA.
XX AC
XX AC AAE23286;
XX DT 27-AUG-2002 (first entry)

```

```

XX Human nectin-3beta protein.
XX DE
XX KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Modified-site 73
FT Domain /note= "N-glycosylated"
FT Modified-site 74..152
FT /note= "Extracellular Ig domain"
FT Modified-site 83
FT /note= "N-glycosylated"
FT Modified-site 125
FT /note= "N-glycosylated"
FT Modified-site 186
FT /note= "N-glycosylated"
FT Domain /note= "N-glycosylated"
FT /note= "Extracellular Ig domain"
FT Modified-site 222
FT /note= "N-glycosylated"
FT Domain /note= "N-glycosylated"
FT Modified-site 331
FT /note= "N-glycosylated"
FT Domain /note= "Intracellular C-terminal domain"
XX WO200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392..
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV ) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37445.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX Claim 1; Page 98-99; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,
XX proliferation or angiogenic condition of a tissue or a subject, such as
XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX stroke, restenosis, tumour growth and treating herpesvirus infection.
XX Nectin is also useful for modulating proliferation or migration of an
XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
XX smooth muscle cell). The present sequence is human nectin-3beta protein.

```


| | | |
|----------|---|--|
| CC | Human nectin-3beta gene is located on chromosome 3 | |
| XX | Sequence 510 AA; | |
| SQL | Query Match Best Local Similarity 99.3%; Score 2693; DB 5; Length 510; Matches 508; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | |
| QY | 1 MARTPGSPPLCPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPPLLLFSLRLCGALAGPI 60 | |
| DB | 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPPLLLFSLRLCGALAGPI 60 | |
| QY | 61 IVEPHVTAVGKNVSKLCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQEGYQGR 120 | |
| DB | 61 IVEPHVTAVGKNVSKLCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQEGYQGR 120 | |
| QY | 121 VLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSQTVTVLVEPTVSLIKGPD 180 | |
| DB | 121 VLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSQTVTVLVEPTVSLIKGPD 180 | |
| QY | 181 LIDGNETVAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPPTPRAR 240 | |
| DB | 181 LIDGNETVAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPPTPRAR 240 | |
| QY | 241 GRRITCVVKHPALEKDIRYSFLDIQYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300 | |
| DB | 241 GRRITCVVKHPALEKDIRYSFLDIQYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300 | |
| QY | 301 KSVMSRLDQWPDGLLASDNLHVFHPLTFNYSGVYICKVNSLQGRSDQKVIISDVVF 360 | |
| DB | 301 KSVMSRLDQWPDGLLASDNLHVFHPLTFNYSGVYICKVNSLQGRSDQKVIISDVVF 360 | |
| QY | 361 KQTSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420 | |
| DB | 361 KQTSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420 | |
| QY | 421 PPLQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSPDYEDENPVGEGDGIQMYPLYN 480 | |
| DB | 421 PPLQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSPDYEDENPVGEGDGIQMYPLYN 480 | |
| QY | 481 QMCYQDRSPGKHQNDPKRYVIDPREHYV 510 | |
| DB | 481 QMCYQDRSPGKHQNDPKRYVIDPREHYV 510 | |
| RESULT 3 | | |
| AAE23284 | | |
| ID | AAE23284 standard; protein; 504 AA. | |
| XX | | |
| AC | AAE23284; | |
| XX | | |
| DT | 27-AUG-2002 (first entry) | |
| XX | | |
| DE | Human deleted nectin-3beta protein. | |
| XX | | |
| KW | Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; | |
| KW | paracellular transport disorder; kidney; diabetic retinopathy; allergy; | |
| KW | allotraft rejection; metastasis; restenosis; inflammatory bowel disease; | |
| KW | oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; | |
| KW | stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3. | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200228902-A2. | |
| XX | | |
| PD | 11-APR-2002. | |
| XX | | |
| PF | 05-OCT-2001; 2001WO-US031392. | |
| XX | | |
| PR | 05-OCT-2000; 2000US-0238557P. | |
| XX | | |
| PA | (IMMUNEX CORP. | |
| XX | | |
| PI | Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A; | |
| XX | WPI; 2002-426103/45. | |
| DR | N-PSDB; AAD37443. | |
| XX | Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, | |
| PT | useful for treating or preventing heart failure, malaria, | |
| PT | glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, | |
| PT | sepsis, stroke. | |
| XX | Claim 1; Page 89-91; 141pp; English. | |
| XX | The invention relates to a substantially purified nectin3alpha, beta, | |
| CC | gamma and nectin-4 polypeptides and their corresponding polynucleotides. | |
| CC | Nectin DNA and protein are useful for treating a disease associated with | |
| CC | cell adhesion activity, adherens junction formation activity, epithelial | |
| CC | or endothelial barrier function activity, endothelial proliferation or | |
| CC | migration activity, viral polypeptide binding activity. The epithelial or | |
| CC | endothelial barrier function disorder which is treated by the above | |
| CC | mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, | |
| CC | asthma, allergy, allotraft rejection, metastasis of cancer cells, | |
| CC | paracellular transport disorders such as magnesium transport defects in | |
| CC | the kidney or inflammatory bowel disease. Nectin DNA is also useful for | |
| CC | inhibiting angiogenesis in a mammal and treating endothelial migration, | |
| CC | proliferation or angiogenic condition of a tissue or a subject, such as | |
| CC | ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, | |
| CC | stroke, restenosis, tumour growth and treating herpesvirus infection. | |
| CC | Nectin is also useful for modulating proliferation or migration of an | |
| CC | endothelial cell, an epithelial cell or a smooth muscle cell (vascular | |
| CC | smooth muscle cell). The present sequence is human nectin-3beta protein | |
| CC | containing 6 amino acids deleted from the N-terminal end. Human nectin- | |
| CC | 3beta gene is located on chromosome 3 | |
| XX | | |
| SQL | Sequence 504 AA; | |
| QY | Query Match 98.8%; Score 2679; DB 5; Length 504; | |
| DB | Best Local Similarity 100.0%; Pred. No. 3.2e-214; Mismatches 0; Gaps 0; | |
| XX | Matches 504; Conservative 0; Indels 0; | |
| QY | 7 PSPLCPGCGGAQKQLSSASLLGAGLLQLQPTPPPLLLLPPLLLFSLRLCGALAGPIIPEHV 66 | |
| DB | 1 PSPLCPGCGGAQKQLSSASLLGAGLLQLQPTPPPLLLLPPLLLFSLRLCGALAGPIIPEHV 60 | |
| QY | 67 TAVWGNVSKLCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGRVLFKNY 126 | |
| DB | 61 TAVWGNVSKLCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGRVLFKNY 120 | |
| QY | 127 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSQTVTVLVEPTVSLIKGPDSDIGGN 186 | |
| DB | 121 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSQTVTVLVEPTVSLIKGPDSDIGGN 180 | |
| QY | 187 ETVAACIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPPTRFARGRITC 246 | |
| DB | 181 ETVAACIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPPTRFARGRITC 240 | |
| QY | 247 VVKHPALEKDIRYSFLDIQYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPFKSVMSR 306 | |
| DB | 241 VVKHPALEKDIRYSFLDIQYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPFKSVMSR 300 | |
| QY | 307 LDGQWPDGLLASDNLHVFHPLTFNYSGVYICKVNSLQGRSDQKVIISDVPFKQTSI 366 | |
| DB | 301 LDGQWPDGLLASDNLHVFHPLTFNYSGVYICKVNSLQGRSDQKVIISDVPFKQTSI 360 | |
| QY | 367 AVAGAVIGAVLALFIIAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERSPPLPQK 426 | |
| DB | 361 AVAGAVIGAVLALFIIAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERSPPLPQK 420 | |
| QY | 427 DLQFQPEHLPLQTFKEREVGNLQHSNGLNSRSPDYEDENPVGEGDGIQMYPLYNQMCYQD 486 | |
| DB | 421 DLQFQPEHLPLQTFKEREVGNLQHSNGLNSRSPDYEDENPVGEGDGIQMYPLYNQMCYQD 480 | |
| QY | 487 RSPGKHQNDPKRYVIDPREHYV 510 | |

```

Db      481 RSPGKHQNDPKRVYIDPREHYV 504
RESULT 4
AAG63983
ID      AAG63983 standard; protein; 510 AA.
XX
XX
AC      AAG63983;
XX
XX      26-NOV-2001 (first entry)
XX
XX      Amino acid sequence of murine nectin-3.
XX
XX      Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
XX
XX      Mus sp.
XX
XX      WO200166736-A1.
XX
XX      13-SEP-2001.
XX
XX      09-MAR-2001; 2001WO-JP001871.
XX
XX      09-MAR-2000; 2000JP-00065595.
XX
XX      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX      (TAKA/) TAKAHASHI K.
XX
XX      Takahashi K, Takai Y, Nakanishi H, Sato K;
XX
XX      WPI; 2001-570771/64.
XX      N-PSDB; AAH78180.
XX
XX      New protein family for diagnosing and treating tumor infiltration and
XX      metastasis comprises the mouse nectin-3 protein families and
XX      corresponding antibodies.
XX
XX      Claim 2; Page 45-48; 64pp; Japanese.
XX
XX      The present sequence represents a murine nectin-3 polypeptide. Nectin-3
XX      is an immunoglobulin-like cell adhesion molecule that shows homophilic
XX      and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
XX      polynucleotides are useful for investigating the mechanisms of cell
XX      adhesion, infiltration and metastasis of cancer cells, the diagnosis of
XX      malignancies of various cancers, and the development of methods for the
XX      treatment and prevention of cancer
XX
XX      Sequence 510 AA;
XX
Query Match      88.7%; Score 2406; DB 4; Length 510;
Best Local Similarity 89.2%; Pred. No. 1.9e-191;
Matches 456; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY      1 MARTPGSPCLPGGKQALSSASLLGALLLOPPTPPPLLLLPFLLLFRLCALAGPI 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MARTPGAPLCPGGKQALSSAFPAPAGLLLPATPPPLLLLPFLLLFRLCALAGSI 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSGVDYQGR 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121 VLFKNYSINDATITLHNIFGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 VLFKNYSINDATITLHNIFGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      181 LIDGNETVAICAAATGKPAHIDWEGDLGEMESTTSPNETATTISQVLPPTFPAR 240
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 LIDGNETVAACVAAATGKPAQDWEGDLGEMESTTSPNETATTISQVLPPTFPAR 240
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      241 GRRITCVVKHPALEKDIRYSFILDIAPEVSVTVTGDNWVFVGRKGNLKNADANPPPF 300
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 GRRITCVVKHPALEKDIRYSFILDIAPEVSVTVTGDNWVFVGRKGNLKNADANPPPF 300
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQOKVIYISDVPF 360
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQOKVIYISDIP 360
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYEERS 420
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 TQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYEERI 420
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 PPLPQKDLF-OPHPLPLOTQFKEREYCNLOHNSLRSRFDYEDENPVGCDGLOQMYPLY 479
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 PSLPQKDLGQTEHLPLOTQFKKGAGLQSPNGPISRRFRDYEDESTMOEDGTQRCMPLY 480
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
480 NMCYQDRSPGKHQNDPKRVYIDPREHYV 510
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 SQMCHQDRSPRQHHPN-PERLYINPREHYV 510
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
AAE23292
ID      AAE23292 standard; protein; 510 AA.
XX
XX      AAE23292;
XX
XX      27-AUG-2002 (first entry)
XX
XX      Mouse nectin-3beta protein.
XX
XX      Mouse; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
XX      paracellular transport disorder; kidney; diabetic retinopathy; allergy;
XX      allograft rejection; metastasis; restenosis; inflammatory bowel disease;
XX      oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
XX      stroke; tumour; cancer; herpesvirus infection; asthma.
XX
XX      Mus musculus.
XX
XX      WO200228902-A2.
XX
XX      11-APR-2002.
XX
XX      05-OCT-2001; 2001WO-US031392.
XX
XX      05-OCT-2000; 2000US-0238557P.
XX      (IMMV ) IMMUNEX CORP.
XX
XX      Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX      WPI; 2002-426103/45.
XX
XX      Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX      useful for treating or preventing heart failure, malaria,
XX      glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX      sepsis, stroke.
XX
XX      Disclosure; Page 109-110; 141pp; English.
XX
XX      The invention relates to a substantially purified nectin3alpha, beta,
XX      gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX      Nectin DNA and protein are useful for treating a disease associated with
XX      cell adhesion activity, adherens junction formation activity, epithelial
XX      or endothelial barrier function activity, endothelial proliferation or
XX      migration activity, viral polypeptide binding activity. The epithelial or
XX      endothelial barrier function disorder which is treated by the above
XX      mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX      asthma, allergy, allograft rejection, metastasis of cancer cells,
XX      paracellular transport disorders such as magnesium transport defects in
XX      the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX      inhibiting or angiogenic condition in a mammal and treating endothelial migration,
XX      proliferation or angiogenesis in a mammal and treating endothelial migration,
XX      ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX      stroke, restenosis, tumour growth and treating herpesvirus infection.
XX      Nectin is also useful for modulating proliferation or migration of an
XX      endothelial cell, an epithelial cell or a smooth muscle cell (vascular

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CC smooth muscle cell). The present sequence is mouse nectin-3beta protein
XX
SQ Sequence 510 AA;

Query Match      88.7%; Score 2406; DB 5; Length 510;
Best Local Similarity 89.2%; Pred. No. 1.9e-191;
Matches 456; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

Qy 1 MARTPGSPSPCPGGKAQLSSASLLGAGLLIQPTPPPLLLLLLFSRLCGALAGPI 60
Db 1 MARTPGAPLCPGGKAQLSSAFPAAGLLLPAPTTPPLLLLLLFSRLCGALAGSI 60

Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYGR 120
Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSGVDYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRPAR 240
Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRPAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTCYDGNWVFGKGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTCYDGNWVFGKGNLKNADANPPPF 300

Qy 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTNYSGVYICKVNSLQGRSDQKVIISDVVF 360
Db 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTNYSGVYICKVNSLQGRSDQKVIISDIPL 360

Qy 361 KQTSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KQTSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERI 420

Qy 421 PPLPKDLF-QPEHLPLQTKEREVGNLQSHNGLSRSPDYEDENPVGEDIQOMVPLY 479
Db 421 PSLPKDLGQTEHLPLQTKPKGAGGLQPSNGIPISRRFDYDESTMQEDGTQMCPPLY 480

Qy 480 NQMVCQRSPGKHQNNNDPKRVYIDPREHYV 510
Db 481 SOMCHQDESPPQHPRN-PERLYINPREHYV 510

RESULT 6
AAE23299
ID AAE23299 standard; protein; 437 AA.
AC AAE23299;
XX
XX 27-AUG-2002 (first entry)
DT
DE Human nectin-3gamma protein.
XX
KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
XX WO200228902-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMUNEX CORP.
XX
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PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37450.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
PS Claim 1; Page 125-126; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
CC Human nectin-3gamma gene is located on chromosome 3
XX
SQ Sequence 437 AA;

Query Match      82.7%; Score 2243; DB 5; Length 437;
Best Local Similarity 99.5%; Pred. No. 5.8e-178;
Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTPGSPSPCPGGKAQLSSASLLGAGLLIQPTPPPLLLLLLFSRLCGALAGPI 60
Db 1 MARTLRSPSPCPGGKAQLSSASLLGAGLLIQPTPPPLLLLLLFSRLCGALAGPI 60

Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYGR 120
Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRPAR 240
Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRPAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTCYDGNWVFGKGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTCYDGNWVFGKGNLKNADANPPPF 300

Qy 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTNYSGVYICKVNSLQGRSDQKVIISDVVF 360
Db 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTNYSGVYICKVNSLQGRSDQKVIISDVVF 360

Qy 361 KQTSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KQTSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420

Qy 421 PPLPKDLFQ 430
Db 421 PPLPKDLFQ 430

RESULT 7
AAG63984
```

ID AAG63984 standard; protein; 438 AA.
 AC AAG63984;
 XX
 XX 26-NOV-2001 (first entry)
 XX
 XX Amino acid sequence of murine nectin-3.
 DE
 XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
 KW
 XX Mus sp.
 OS
 XX WO200166736-A1.
 PN
 XX 13-SEP-2001.
 PD
 XX 09-MAR-2001; 2001WO-JP001871.
 XX
 XX 09-MAR-2000; 2000JP-00065595.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX (TAKA/) TAKAHASHI K.
 PA
 XX Takahashi K, Takai Y, Nakanishi H, Sato K;
 PI
 XX WPI; 2001-570771/64.
 DR
 XX N-PSDB; AAH78181.
 DR
 XX New protein family for diagnosing and treating tumor infiltration and
 PT metastasis comprises the mouse nectin-3 protein families and
 PT corresponding antibodies.
 PT
 XX Claim 3; Page 53-55; 64pp; Japanese.
 PS
 XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3
 CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
 CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
 CC polynucleotides are useful for investigating the mechanisms of cell
 CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
 CC malignancies of various cancers, and the development of methods for the
 CC treatment and prevention of cancer
 XX
 XX Sequence 438 AA;
 SQ
 Query Match 78.4%; Score 2125; DB 4; Length 438;
 Best Local Similarity 93.7%; Pred. No. 4e-168;
 Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MARTPGSPPLCPGGKQALSSALLGAGLLLOPPTPPLLLLPPLLLFSLRCLGALAGPI 60
 DB 1 MARTPGPAPLCPGGKQALSSAFPAPAGLLLPAPTTPPLLLLPPLLLFSLRCLGALAGSI 60
 QY 61 IVEPHVAVMGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFSGVQGR 120
 DB 61 IVEPHVAVMGKNSVLSKCLIEVNETITQISWEKIHGKSTQVAVHPQYGFSGVQGR 120
 QY 121 VLFKNYSINDATITLHNIGSDSKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSINDATITLHNIGSDSKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAICTAATGKPAHIDWEGDLGEMESTTSPNETATIIISQVKLPPTRFAR 240
 DB 181 LIDGGNETVAICVAAATGKPAQIDWEGDLGEMESTTSPNETATIVSQVKLPPTRFAR 240
 QY 241 GRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
 DB 241 GRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
 QY 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSQVYICKVTNSLQGRSDQKVIYISDVPF 360
 DB 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSQVYICKVTNSLQGRSDQKVIYISDIP 360
 QY 361 KOTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRKPSYLDKVIDLPPTHKPPPLYEERS 420

Db 361 TQISSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRKPSYLDKVIDLPPTHKPPVYERI 420
 QY 421 PPLPQKDL 428
 | | | | |
 Db 421 PSLPQKDL 428
 | | | | |
 RESULT 8
 AAE23293
 ID AAE23293 standard; protein; 438 AA.
 XX
 AC AAE23293;
 XX
 DT 27-AUG-2002 (first entry)
 DE
 XX Mouse nectin-3gamma protein.
 XX
 KW Mouse; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma.
 XX
 OS Mus musculus.
 XX
 XX WO200228902-A2.
 PN
 XX 11-APR-2002.
 PD
 XX 05-OCT-2001; 2001WO-US031392.
 PF
 XX 05-OCT-2000; 2000US-0238557P.
 PR
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 PI
 XX WPI; 2002-426103/45.
 XX
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 PT
 XX Disclosure; Page 111-112; 141pp; English.
 XX
 XX The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is mouse nectin-3gamma protein
 XX
 SQ Sequence 438 AA;
 Query Match 78.4%; Score 2125; DB 5; Length 438;
 Best Local Similarity 93.7%; Pred. No. 4e-168;
 Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MARTPGSPPLCPGGKQALSSALLGAGLLLOPPTPPLLLLPPLLLFSLRCLGALAGPI 60

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Db 1 MARTPGAPLCPGGKQAQLSSAAPPAGALLPAPTTPPLLLLLLPLLFRLCGALAGSI 60
Qy 61 IVEPHVTAVWGKQVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVWGKQVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDAITTLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDAITTLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Qy 241 GRITCVVHKPALEKDIRYFILDIOYAPEVSVTYGDNMFVGRKGNLKNADANPPPF 300
Db 241 GRITCVVHKPALEKDIRYFILDIOYAPEVSVTYGDNMFVGRKGNLKNADANPPPF 300
Qy 301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 360
Db 301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 360
Qy 361 KOTSSIAVAGAVIGAVLALFIIAIFVTVLTTPRKRPSTYLDKVIDLPTTHKPPPLYBERS 420
Db 361 KOTSSIAVAGAVIGAVLALFIIAIFVTVLTTPRKRPSTYLDKVIDLPTTHKPPPLYBERS 420
Qy 421 PPLPQKDL 428
Db 421 PPLPQKDL 428

```

RESULT 9

AAE23288
ID AAE23288 standard; protein; 595 AA.

AC AAE23288;

XX 27-AUG-2002 (first entry)

XX Human nectin-3beta-IgG1Fc region fusion protein.
XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.

OS Homo sapiens.

OS Unidentified.

OS Chimeric.

XX WO200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 9; Page 102-104; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;

Query Match 71.3%; Score 1932; DB 5; Length 595;

Best Local Similarity 86.8%; Pred. No. 7.6e-152;

Matches 375; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

Qy 1 MARTPGSPPLCPGGKQAQLSSALLGAGLLLQPPPTPPLLLLLLPLLFRLCGALAGPI 60

Db 1 MARTPGSPPLCPGGKQAQLSSALLGAGLLLQPPPTPPLLLLLLPLLFRLCGALAGPI 60

Qy 61 IVEPHVTAVWGKQVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120

Db 61 IVEPHVTAVWGKQVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120

Qy 121 VLFKNYSLNDAITTLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180

Db 121 VLFKNYSLNDAITTLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240

Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240

Qy 241 GRITCVVHKPALEKDIRYFILDIOYAPEVSVTYGDNMFVGRKGNLKNADANPPPF 300

Db 241 GRITCVVHKPALEKDIRYFILDIOYAPEVSVTYGDNMFVGRKGNLKNADANPPPF 300

Qy 301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 360

Db 301 KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 360

Qy 361 KOTSSIAVAGAVIGAVLALFIIAIFVTVLTTPRKRPSTYLDKVIDLPTTHKPPPLYBERS 420

Db 361 KOTSSRS-----CDK-----THTCPCPAPEA 382

Qy 421 PPLPQKDLFOPE 432

Db 383 EGAPSVLFPFK 394

RESULT 10

AAE23290

ID AAE23290 standard; protein; 387 AA.

XX AAE23290;

XX 27-AUG-2002 (first entry)

XX Human nectin-3beta-FLAGpolyHis fusion protein.

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW

| | |
|-----------|--|
| CC | Human nectin-3alpha gene is located on chromosome 3 |
| XX | |
| SQ | Sequence 549 AA; |
| | Query Match 70.3%; Score 1906.5; DB 5; Length 549; Best Local Similarity 67.6%; Pred. No. 9e-150; Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10; |
| QY | 1 MARTPGSPPLCGGKAQLSSASLLGAGLLLPPTPPPLLLLLLFPFLLSRLCGLAGPI 60 Db 1 MARTLRPSPLCGGKAQLSSASLLGAGLLLPPTPPPLLLLLLFPFLLSRLCGLAGPI 60 |
| QY | 61 IVEPHVTAVWGNVSKLCLEIENETITQISWEKIHGKSQTVAVHHPOYGFSVGGEYQGR 120 Db 61 IVEPHVTAVWGNVSKLCLEIENETITQISWEKIHGKSQTVAVHHPOYGFSVGGEYQGR 120 |
| QY | 121 VLFKNYSLNDAITILHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVPEPVSIIKGPD 180 Db 121 VLFKNYSLNDAITILHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVPEPVSIIKGPD 180 |
| QY | 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTTFPNETATIISQYKLPTFPAR 240 Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTTFPNETATIISQYKLPTFPAR 240 |
| QY | 241 GRRTICVVKHPALEKDRIYSFILDIQYAPEVSVTYDGNWFVGRGVNKKCNADANPPP 300 Db 241 GRRTICVVKHPALEKDRIYSFILDIQYAPEVSVTYDGNWFVGRGVNKKCNADANPPP 300 |
| QY | 301 KSWNSRLDGQWPDGLLASDNTHLVHPLTFNYSGVIKVNTSLGQRSDDQKIIVISDPV- 359 Db 301 KSWNSRLDGQWPDGLLASDNTHLVHPLTFNYSGVIKVNTSLGQRSDDQKIIVISDPPT 360 |
| QY | 360 -----FKOTSSIAVAGAVICAVLALFIIA 383 361 TTTLTQPTIOWHFSTADIEDLATEPKPLPPLSTLATIKDDTIATIIASVWGALFIVLVS 420 384 IFVTVLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPPLP 424 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQESQIDVLQDELDSYDPSVKKENKPNV- 478 425 QKDLFOPEHL--PLQTFKEREVGNLQHNSNGLSRFSFYEDENPVGEDGIQQMYPVLYNQ 482 479 -NNLIRKDYLEEPEKTOW----NNVENLNRF-ERPMDYYEDLKMGKFVSD----- 523 483 CYQDRSPGKHQNNDPRV-----YIDPREHYV 510 524 -----EHYDENEDDLVSHVDGVSISRREWYV 549 |
| RESULT 13 | |
| ABU20222 | ID ABU20222 standard; protein; 549 AA. |
| XX | AC ABU20222; |
| XX | DT 13-AUG-2003 (first entry) |
| DE | Human IG gene related protein SEQ ID No 45. |
| XX | Breast cancer; p53 pathway modulating agent; IG; colon cancer; |
| KW | kidney cancer; lung cancer; ovary cancer; human. |
| OS | Homo sapiens. |
| XX | WO200299040-A2. |
| FN | 12-DEC-2002. |
| PD | 03-JUN-2002; 2002WO-US017313. |
| PF | 05-JUN-2001; 2001US-0296076P. |
| XX | 10-OCT-2001; 2001US-0328605P. |
| PR | 22-OCT-2001; 2001US-0338733P. |

Qy 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
Db 524 -----EYDENEEDLVSHVDGVSISRREWYV 549

RESULT 14
ADR66369
ID ADR66369 standard; protein; 549 AA.

XX AC ADR66369;
XX DT 02-DEC-2004 (first entry)
XX DE Human prostatic carcinoma derived protein SEQ ID 223 #2.

XX KW human; cytostatic; diagnosis; prostatic cancer;
XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX XX 22-FEB-2004; 2004WO-DE000433.

XX PF 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX XX (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX WPI; 2004-653386/63.

XX PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
agents.

XX PS Claim 2; Page 703; 1607pp; German.
XX CC This invention describes novel cytostatic polynucleotide and polypeptide
sequences which can be used in a method for diagnosing prostatic cancer
or the risk of developing prostatic cancer. Diagnosis is based on
determining over transcription or over expression of the sequences in
prostatic tissue. Screening for inhibitors of the sequences or detection
substances involves a binding assay, any compounds that bind are
selected, optionally after deconvolution of mixtures. Detection of a
predetermined minimum level of the reporter indicates the presence of a
tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
short-interfering RNA or ribozymes; an organic molecule of molecular
weight below 5000, preferably 300, that binds to the polypeptide; an
aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
polypeptide, preferably humanised or human; an anti-idiotype, non-human
(monoclonal) antibody directed against Ab or any of the above derivatised
with a reporter group, cell toxin, immunostimulatory molecules and/or
radioisotope. The polynucleotides are identified in human prostatic
cancer by differential expression analysis, using DNA microarrays,
between normal and tumorous tissues, with (over)expression being detected
by quantitative PCR. Analysis of prostatic cancer samples showed that
CD24 was upregulated in many of them. Sections of tissue, isolated from
prostatic cancer patients, or subjects at risk, were incubated
sequentially with anti-human CD4 murine monoclonal antibodies;
biotinylated second antibody; streptavidin-conjugated horseradish
peroxidase and then diaminobenzidine as colour former (brown). The
samples were counterstained with hemalum (blue). Malignant cells stained

CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.

XX SQ Sequence 549 AA;

Query Match 70.3%; Score 1906.5; DB 8; Length 549;
Best Local Similarity 67.6%; Pred. No. 9e-150;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;

Qy 1 MARTPGSPLCGCGKAQLSSASLGGALLGLOPPTPPPLALLLPPLLLFRLCGALAGPI 60

Db 1 MARTLPSPLCPGCGKAQLSSASLGGALLGLOPPTPPPLALLLPPLLLFRLCGALAGPI 60

Qy 61 IVSPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYQSFVSGEYQGR 120

Db 61 IVSPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPQYQSFVSGEYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVETVSLIKGPD 180

Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVETVSLIKGPD 180

Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQKLPPTFRAR 240

Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQKLPPTFRAR 240

Qy 241 GRRITCVVHKPALEKDIRYSFILDIOVAPEVSVTVGDNWFGVGRKGNLKNADANPPFP 300

Db 241 GRRITCVVHKPALEKDIRYSFILDIOVAPEVSVTVGDNWFGVGRKGNLKNADANPPFP 300

Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYGVIKVTNSLGQSDQKVIYISDVP- 359

Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYGVIKVTNSLGQSDQKVIYISDVP- 360

Qy 360 -----FKQTSSAVAGAVTAVLALFIIA 383

Db 361 TTTLOPTIOWHPSTADIEDLATEPKLPFLSTLATIKDDTIATIIASVVGALFIVLVS 420

Qy 384 IFVTLLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424

Db 421 VLAGIFCYRRRTFRGDFYFKNY-IPPSDMQKESQIDVLQOEDLSDSPDSVKKNKPNV- 478

Qy 425 QKDLFQPEHL--PLQTFKEREVENLQHSNGLNSRSPDYEDENPVVGEDGIQQMYPLYNQM 482

Db 479 -NNLIRKDYLEEPEKTQW-----NNVENLNR-ERPMDYVEDLKMGMKFVSD----- 523

Qy 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510

Db 524 -----EYDENEEDLVSHVDGVSISRREWYV 549

RESULT 15

ADR66711

ID ADR66711 standard; protein; 549 AA.

XX AC ADR66711;

XX DT 02-DEC-2004 (first entry)

XX DE Human prostatic carcinoma derived protein SEQ ID 223 #3.

XX KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

```

XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
XX (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Kinzhong L, Staub E;
XX WPI; 2004-653386/63.
XX
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 2; Page 1205; 1607pp; German.
XX
XX This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
XX invention.
XX
SQ Sequence 549 AA;
Query Match 70.3%; Score 1906.5; DB 8; Length 549;
Best Local Similarity 67.6%; Pred. No. 9e-150;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;
QY 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
DB 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
QY 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEYQGR 120
DB 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEYQGR 120
QY 121 VLFKNYSINDATITLHNI GFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPD 180
DB 121 VLFKNYSINDATITLHNI GFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPD 180
QY 181 LIDGNETVAATCAATGKPVAHIDWEGDLGEMESTTTSPNETATTISQYKLPPTRFAR 240

```

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DB 181 LIDGNETVAATCAATGKPVAHIDWEGDLGEMESTTTSPNETATTISQYKLPPTRFAR 240
QY 241 GRRITCVVKHPALEKDIRYSPFLDIQYAPEVSVTGYDGNWFFVGRKGVNLKCNADANPPPF 300
DB 241 GRRITCVVKHPALEKDIRYSPFLDIQYAPEVSVTGYDGNWFFVGRKGVNLKCNADANPPPF 300
QY 301 KSVWSRLDGQWPDGGLASDNTLHFVHPLTFTNYSVVYICKVTSLSGQSDQKVYIISDVP 359
DB 301 KSVWSRLDGQWPDGGLASDNTLHFVHPLTFTNYSVVYICKVTSLSGQSDQKVYIISDPP 360
QY 360 -----FKQTSIAVAGAVIGAVLALFIA 383
DB 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPPLSLATIKDDTIATIIASVVGALFIVLS 420
QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPLYEERSPELP 424
DB 421 VIAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYPSVKKENKPNV- 478
QY 425 QKDLFOPEHL--PLOTQFKEREVGNLQHSNLSRSFDYEDENPNVGEDGTQQMYPLYNQM 482
DB 479 -NNLRKDYLEBPEKTQW-----NNVENLNR-ERPMDYIEDLKMGMKFVSD----- 523
QY 483 CYQDRSPGKHQNNDPKRV-----YIDPREHVV 510
DB 524 -----EHDYDENEEDLVSHVDGSGVISRREWYV 549

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Search completed: October 6, 2005, 09:51:34
Job time : 86.2348 secs

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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:42:42 ; Search time 16.7671 Seconds
(without alignments)
2926.593 Million cell updates/sec

Title: US-09-972-268-10
Perfect score: 2711
Sequence: 1 MARIPTGPSPLCPGGKQALS.....KHQNDPKRYIDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 1173.5 | 43.3 | 407 | 2 T08732 | hypothetical prote |
| 2 | 565.5 | 20.9 | 518 | 2 JC4024 | poliovirus recepto |
| 3 | 540 | 19.9 | 530 | 2 A53437 | poliovirus recepto |
| 4 | 527 | 19.4 | 538 | 2 I68093 | PRR2 delta - human |
| 5 | 467 | 17.2 | 467 | 1 HJMSF3 | poliovirus recepto |
| 6 | 455 | 16.8 | 478 | 2 I53960 | PRR2 alpha - human |
| 7 | 418 | 15.4 | 392 | 2 B44194 | poliovirus recepto |
| 8 | 418 | 15.4 | 417 | 2 A44194 | poliovirus recepto |
| 9 | 402 | 14.8 | 392 | 1 RWHUPD | poliovirus recepto |
| 10 | 402 | 14.8 | 417 | 1 RWHUPA | poliovirus recepto |
| 11 | 326.5 | 12.0 | 416 | 2 A54017 | colon carcinoma-as |
| 12 | 229.5 | 8.5 | 764 | 2 A49448 | irregular chiasm C |
| 13 | 204.5 | 7.5 | 4391 | 2 A38096 | perlecan precursor |
| 14 | 196.5 | 7.2 | 5175 | 2 T20992 | hypothetical prote |
| 15 | 186.5 | 7.2 | 5198 | 2 T43290 | hemicentin precurs |
| 16 | 187.5 | 6.9 | 274 | 2 A47639 | OX-2 membrane glyco |
| 17 | 181.5 | 6.7 | 1896 | 2 T08851 | Down syndrome cell |
| 18 | 178 | 6.6 | 588 | 2 JH0506 | adhesion molecule |
| 19 | 178 | 6.6 | 588 | 2 A45254 | surface glycoprote |
| 20 | 177.5 | 6.5 | 853 | 1 LJBOHC | neural cell adhesi |
| 21 | 177 | 6.5 | 626 | 1 A61084 | myelin-associated |
| 22 | 177 | 6.5 | 637 | 2 B33785 | myelin-associated |
| 23 | 176 | 6.5 | 7962 | 2 T38346 | elastic titin - hu |
| 24 | 175 | 6.5 | 582 | 1 BNRT3S | myelin-associated |
| 25 | 175 | 6.5 | 626 | 1 BNRT3 | myelin-associated |
| 26 | 174 | 6.4 | 1091 | 2 A58532 | glial cell membran |
| 27 | 172.5 | 6.4 | 3707 | 2 S18252 | heparan sulfate pr |
| 28 | 170.5 | 6.3 | 365 | 2 JC7780 | coxsackie- and ade |
| 29 | 164.5 | 6.1 | 847 | 2 JH0371 | B-cell adhesion pr |

30 162.5 6.0 278 1 TDRTOX
31 162.5 6.0 858 1 IJRTNC
32 162 6.0 587 2 JH0464
33 162 6.0 761 1 IJHUNG
34 162 6.0 765 2 C42632
35 162 6.0 812 2 B42632
36 162 6.0 932 2 A42632
37 161.5 6.0 739 2 JN0581
38 160.5 5.9 702 2 A36319
39 160 5.9 725 1 IJMSNG
40 157 5.8 509 2 JC5288
41 157 5.8 1091 1 IJCHNL
42 156 5.8 646 2 I38049
43 155 5.7 513 2 JC5289
44 154 5.7 1612 2 T30805
45 153.5 5.7 1051 2 A39712

ALIGNMENTS

RESULT 1

T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08732
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OTT>
A:Cross-references: UNIPROT:Q9Y412; EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZp566B0846
C:Genetics:
A:Note: DKFZp566B0846.1

Query Match 43.3%; Score 1173.5; DB 2; Length 407;
Best Local Similarity 62.8%; Pred. No. 9.2e-79;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Qy 143 SGKICAVTFPIGNAQSSTTVLVPTVSLIKGPDLSLDGNETVAAICIAATGKPA 202
Db 1 SGKICAVTFPIGNAQSSTTVLVPTVSLIKGPDLSLDGNETVAAICIAATGKPA 60
Qy 203 HIDWEGDLGEMESTTTSFPNETATIIISOYKLPPTFARGRITCVVKHPALEKDIRYSFI 262
Db 61 HIDWEGDLGEMESTTTSFPNETATIIISOYKLPPTFARGRITCVVKHPALEKDIRYSFI 120
Qy 263 LDIOYAPEVSVTGDNWFGVRKGVNLKCNADANPPFPKSVWSRLDGOWPDGLLASDNTL 322
Db 121 LDIOYAPEVSVTGDNWFGVRKGVNLKCNADANPPFPKSVWSRLDGOWPDGLLASDNTL 180
Qy 323 HFVHPLFTNYSVGVYICKVTSNLGORSQDKYIISDVP----- 359
Db 181 HFVHPLFTNYSVGVYICKVTSNLGORSQDKYIISDPTTTTLQPTIQWHPSTADIEDLAT 240
Qy 360 -----FKQTSSIAVAGAVIGAVLFIATFVTVLLTRKK--RPSYLDKV 403
Db 241 EPKKLPFLSTLATIKDDTIATISVGGALFVLVSLAGIFCYRRRTFRGDFYAKN 300
Qy 404 IDLPPTH-----KPPLYEERSPPLPQKDLFQPBHL--PLQTPQKEREVG 446
Db 301 Y-IPSPDMQKESQIDVLQDELDYFDPVSVKKNPNVNLIRKDYLEPEPTQW-----N 354
Qy 447 NLQHSNGLNSRSDYEDENPVG 468
Db 355 NVENLNRF-ERPMDYEDLKMG 375

RESULT 2

JC4024

Query Match 19.4%; Score 527; DB 2; Length 538;

Best Local Similarity 27.3%; Pred. No. 5.4e-31;
Matches 151; Conservative 94; Mismatches 206; Indels 102; Gaps 21;

QY 33 PPTPPPLLLLLFLLLSRL-CGALAGPIIVEPHVTAVMGKNSLKCLI---EVNETITQ 88
|||:|||||
DB 13 PPIP-----LLWPLLLLLLLETGAQDVRVQVLFVVRGQLGGTVLPCPLLPPVGLYISL 67
|||:|||||
QY 89 ISWEKHGKSS-QTVAVHHPOYGFSGVEGQ--RVLF-----KNYSNDATITL 135
|||:|||||
DB 68 VTWQRPDAPAHQNVAAFPKMGFPSPFPGSERLSFVSAKQSTGQDTAEALQDATAL 127
|||:|||||
QY 136 HNTGFDGSKYICKAVTFPLNGAQSSTVTVLVEP-----TVSLIKGSDSLIDGGNET 188
|||:|||||
DB 128 HGLTVEDEGNYTCEFATPPKSGVRGTMWLRVIAKPKQAEAKVTFSDP-----T 178
|||:|||||
QY 189 VAAICIAATGKPAHI-----DWEGDLGEMESTTTTFPNETATIIISQYKLFPTFRFARGR 242
|||:|||||
DB 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLG---TWTVTSRFTLVFSGRADGV 234
|||:|||||
QY 243 RITCVVHPALEKDIRVSFILDQYAEVSVTVGDGNFVGRKGVNLKCNADANPPPFKS 302
|||:|||||
DB 235 TVTCKVHEGSEFEPALIPVTLVSRYPEVSIISGIDNNWYLGRTDATALCSDVRNSNPETGY 294
|||:|||||
QY 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSODKVIYISDVVPFKQ 362
|||:|||||
DB 295 DWSTTSGTFTPSAVAQGSQ-L-VIHAVDSLNTFTVCTVNAVGMGRABQVIFRET-P-N 351
|||:|||||
QY 363 TSSITAVAGAVIGALALFI-IAIFVTVLLTPRKKRPSYL-----DKVIDLPTTHKPP-P 414
|||:|||||
DB 352 TAGNATGGIIGIIAIIATANAATGILICRQKQEQTLQGAEEDELSGFSYKFPPT 411
|||:|||||
QY 415 LYBERSPLPKQ--DLFPQPHLPLQTOF-----KEREVGNLQHSNG----- 453
|||:|||||
DB 412 KAKLEAQEMPSQLFTLGASEHSPLKTFYFAGASCCTEQEMPRYHFLTLEERSGPLHPGA 471
|||:|||||
QY 454 -----LNSRSDFYED--ENPVGEDGIQOMYPLYNOMCYQDERSPKGHQND 497
|||:|||||
DB 472 TSLGSPIPVPPGPAVEDVDLDEGESEBYLDKINPIYDALSYS--SPSDSYQG-- 527
|||:|||||
QY 498 PKRYVIDPREHYV 510
|||:|||||
DB 528 --KGFVNSRMYV 538
|||:|||||

RESULT 5
HLMSp3
poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A38211
R:Morrisson, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re-
A:Reference number: A38211; MUID:92219365; PMID:1560525
A:Accession: A38211
A:Molecule type: DNA
A:Residues: 1-467 <MOR>
A:Cross-references: UNIPROT:P32507; GB:M80206; NID:G199785; PIDN:AAA39734.1; PID:G199786
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:47-133/Domain: immunoglobulin homology <IMW1>
F:167-231/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM3>
F:355-374/Domain: transmembrane #status predicted <TMN>
F:375-467/Domain: intracellular #status predicted <INT>
F:54-131,174-229,274-320/Disulfide bonds: #status predicted
F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 467; DB 1; Length 467;
Best Local Similarity 32.5%; Pred. No. 1.2e-26;

F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-392/Product: poliovirus receptor delta #status predicted <MAT>
F;21-343/Domain: extracellular #status predicted <EXT>
F;42-125/Domain: immunoglobulin homology <IMM1>
F;159-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-392/Domain: intracellular #status predicted <INT>
F;49-123,166-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 14.8%; Score 402; DB 1; Length 392;
Best Local Similarity 29.3%; Pred. No. 5.7e-22;
Matches 106; Conservative 67; Mismatches 163; Indels 26; Gaps 11;

Qy 44 FPLLLFRLCGAL----AGPIIVE--PHVTAVMGKNSLKLIEVNET----ITQISWEK 93
Db 9 WPLLLVALLVSWPPPGTGVVQAPQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWTR 68

Qy 94 IHGKSSQTVAHH---PQYGFVQGEYQGRVLFKNYSLNDAITITLHNIGFSDSGKIYCKA 150
Db 69 -HGEGSGMAVFHQQTGPSYSESKLEFVAARL--GAELRNASLRFGLRVEDEGNYTCLF 125

Qy 151 VTPPLGNAQSTTTVTLVLEP--TVSLIKGPDLSIDGNETVAACIAATGKPVAHIDWEG 208
Db 126 VTFPQGSRSVDIWLRLVLAKEPONTAEVQVQLT---GEPVPMARCVSTGGRPPAQITWHS 181

Qy 209 DLGEMESTT--TSPNENATIIISQYKLFPTFRFARGRITCVVHKPALEKDIRYSFILDIO 266
Db 182 DLGEMPTNSQVPGFLSGTIVTSLWILVPSQVDGKNVCKVEHSEKPKQLLTVNLTVY 241

Qy 267 YAPEVSVTGVDGNWFGKRGVNLKCNADANPPPKSVWSRLDGOWPDGLASDNLTHFVH 326
Db 242 YPEVSVISGVDNNWYLGQNEATLTCDARSNPEPTGYNWSMTMGLPFPFAVQAGQL-LIR 300

Qy 327 PLTFNYSGVYICKVNTSLGQRSQDKVIYISDVPFKOTSSIAVAGAVICAVLAFIIAIFV 386
Db 301 PVDKPINTTILCNVTNMGALGARQALVTQVKEGPPSEHSGMS-RNAIIFLVILGILVFLILL 359

Qy 387 TV 388
Db 360 GI 361

RESULT 10
RWHPA
poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S12048; A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Izuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: S12048
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA454
A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: A31496
A;Molecule type: mRNA
A;Residues: 1-66, 'A', 68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C;Genetics:
A;Gene: GDB:PVR; PVS

A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <PVR>
F;21-343/Domain: extracellular #status predicted <EXT>
F;42-123,166-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 14.8%; Score 402; DB 1; Length 417;
Best Local Similarity 29.3%; Pred. No. 6.2e-22;
Matches 106; Conservative 67; Mismatches 163; Indels 26; Gaps 11;

Qy 44 FPLLLFRLCGAL----AGPIIVE--PHVTAVMGKNSLKLIEVNET----ITQISWEK 93
Db 9 WPLLLVALLVSWPPPGTGVVQAPQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWTR 68

Qy 94 IHGKSSQTVAHH---PQYGFVQGEYQGRVLFKNYSLNDAITITLHNIGFSDSGKIYCKA 150
Db 69 -HGEGSGMAVFHQQTGPSYSESKLEFVAARL--GAELRNASLRFGLRVEDEGNYTCLF 125

Qy 151 VTPPLGNAQSTTTVTLVLEP--TVSLIKGPDLSIDGNETVAACIAATGKPVAHIDWEG 208
Db 126 VTFPQGSRSVDIWLRLVLAKEPONTAEVQVQLT---GEPVPMARCVSTGGRPPAQITWHS 181

Qy 209 DLGEMESTT--TSPNENATIIISQYKLFPTFRFARGRITCVVHKPALEKDIRYSFILDIO 266
Db 182 DLGEMPTNSQVPGFLSGTIVTSLWILVPSQVDGKNVCKVEHSEKPKQLLTVNLTVY 241

Qy 267 YAPEVSVTGVDGNWFGKRGVNLKCNADANPPPKSVWSRLDGOWPDGLASDNLTHFVH 326
Db 242 YPEVSVISGVDNNWYLGQNEATLTCDARSNPEPTGYNWSMTMGLPFPFAVQAGQL-LIR 300

Qy 327 PLTFNYSGVYICKVNTSLGQRSQDKVIYISDVPFKOTSSIAVAGAVICAVLAFIIAIFV 386
Db 301 PVDKPINTTILCNVTNMGALGARQALVTQVKEGPPSEHSGMS-RNAIIFLVILGILVFLILL 359

Qy 387 TV 388
Db 360 GI 361

RESULT 11
A54017
colon carcinoma-associated antigen p84 precursor - rat
N;Alternate names: p84 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: A54017; A61206
R;Chadaneau, C.; LeMoullac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994
A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinom
A;Reference number: A54017; MUID:94253144; PMID:8195207
A;Accession: A54017
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <CHA>
A;Cross-references: UNIPROT:Q7M048; GB:L12025
R;Chadaneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.
Int. J. Cancer 47, 903-908, 1991
A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcin
A;Reference number: A61206; MUID:91184910; PMID:2010233
A;Accession: A61206
A;Molecule type: protein
A;Residues: 34-41, 'X', 43-53 <CH2>

A;Accession: B33625
A;Molecule type: protein
A;Residues: 1379-1384, 'X', 1386-1388, 'X', 1390-1398 <HE2>
A;Accession: A33625
A;Molecule type: protein
A;Residues: 2166-2171, 'X', 2173-2175, 'X', 2177-2185 <HE3>
A;Note: peptide potentially matches four different regions of sequence shown
C;Genetics:
A;Gene: GDB:HSPG2
A;Cross-references: GDB:126372; OMIM:142461
A;Map position: lp36.1-lp36.1
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrane
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-4391/Product: perlecan #status predicted <MAT>
F:22-193/Domain: I <DOM1>
F:194-530/Domain: II <DOM2>
F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:531-1676/Domain: III <DOM3>
F:1159-1206/Domain: laminin-type EGF-like homology <LEG>
F:1563-1610/Domain: laminin-type EGF-like homology <LEG2>
F:1613-1668/Domain: laminin-type EGF-like homology <LEG3>
F:1677-3686/Domain: IV <DOM4>
F:2007-2034/Domain: transmembrane #status predicted <TRM>
F:3687-4391/Domain: V <DOM5>
F:3845-3880/Domain: EGF homology <EGF1>
F:3888-3921/Domain: EGF homology <EGF>
F:3953-4106/Domain: laminin G repeat homology <LG2>
F:4147-4175/Domain: EGF homology <EGF2>
F:4149-4151/Region: motor neuron attachment (L-R-E) motif
F:4299-4301/Region: motor neuron attachment (L-R-E) motif
F:65.71.76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F:89.554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (covalent)
F:2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 7.5%; Score 204.5; DB 2; Length 4391;
Best Local Similarity 24.1%; Pred. No. 5.1e-06;
Matches 89; Conservative 58; Mismatches 150; Indels 73; Gaps 18;

Qy 8 SPLCPGGKQAQLS-SASLLGAGLL--LQPTPPPLLLLLFFLLFSRLCGALAGIIVE- 63
Db SPADSGEYSCQVTGSSGTLASVLVITIEPSGPI-----PAPGLAQPIYIEA 2931

Qy 64 --PHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGRV 121
Db SSSHVTE--GQTLDLNLCVVP-GQAHQVTVYKRG-----SLPARHQTHG----- 2973

Qy 122 LFKNYSLNDATITLHNGFSDSGKYICAVTFPLGNAGSSTTVT-----LVETV 172
Db -----SQLRLHLVSPADSGEYVCRAAGSGPGQEASFTVTPPSEGSSYRLRGPVI 3024

Qy 173 SLIKGPSLDGGNETVNAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYK 232
Db S-IDPPSSTVOQGQD-ASFKLHIDGAAPISLEWKTRNQLNEDNVHISPN--GSIIT--- 3077

Qy 233 LFPTRFARGRITCVKHPALEKDIRYSFI-LDIQYAPEVSVTVGDNWFGVGRKGNLKC 291
Db IVGTRPSNHGTYRCVASN---AYGVAQSVNLSVHGPTVSVLPGEFVWVKVGAIVLEC 3134

Qy 292 NADANPPFPKSVWRDLG-----QWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNLSG 345
Db -----VSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTVVCLQAQNALG 3192

Qy 346 QRSQDKVIYI 355
Db 3193 TAAQQVEVIV 3202

RESULT 14
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20992; T24733
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20992
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WIL2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
C;Genetics:
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 12512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1

Query Match 7.2%; Score 196.5; DB 2; Length 5175;
Best Local Similarity 26.4%; Pred. No. 2.5e-05;
Matches 88; Conservative 42; Mismatches 138; Indels 65; Gaps 19;

Qy 59 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGE 116
Db PTIESEPHTVNRIERQVTLQCL-AVGIPPEIEWQK--GNVLATLNNPRYTQLADG- 847

Qy 117 YQGRVLFNYSLNDATITLHNGFSDSGKYICAVTFPLGNAGSSTT--VTVLVEPTVSL 174
Db 848 -----NLLITDAQI-----EDQQTCTIARN-TYQQSQSTTMTVLTGLVSPVLGH 891

Qy 175 IKGPSLDGGNETVNAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLF 234
Db VPPEQLIEQDUTLS--CVVLGTTPKPSIWIKDDRPVE-----GPTIKIEGGGSL 943

Qy 235 PTRFARG--RITCVKHPALEKDIRYSFIL-----DIQYAPE-----VSVTYDGNW- 280
Db RLGRGNPKDSGKYTCIAVSPAGNSTLHNVQLIKKPFVYKPEGIVFKPTISGDEKHV 1003

Qy 281 -----FVGRKGNLKCNDANPPFPKSVWRDLGQWP-----DGLLASDNTLHFVH 326
Db AVNSTHVDLDGEGFAIPCVVSGTTPPI-ITW-YLDGR-PITPNSRDFVTADNTL-IVR 1059

Qy 327 PLTFNYSGVYICKVTNLSGORSQDKVIYISDVP 359
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMWNP 1092

RESULT 15
T43290
hemecentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43290; T20993; T24734
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemecentin is required for hemidesmosome mediated cell adhesion and germ
A;Reference number: Z22396
A;Accession: T43290
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20993

A;Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A:Residues: 1-5198 <WIL>

A/RESIDUES: 1-3198 <WILD>
A:Cross-references: EMBL:Z47068: PIDN:CAA87336.1: GSPDB:GN00028: CESP:F15G9.4b

A: Cross-References: EMBL: Z47068; F
A: Experimental source: clone F15G9

A; Experimenta
R: Kershaw, J.

R/Kershaw, J.
submitted to the EMBL Data Library, December 1994

A:Reference number: Z19929

A;Reference Number: T24734

A;ACCESSION: 124734
A:Status: preliminary: translated from GB/EMBL/DDBJ

A:status: preliminary
A:Molecule type: DNA

A;Molecule type: DNA
A:Residues: 1-5198 <WI2>

A;Residues: I-5198 <W12>
A:Cross-references: EMBL:Z47070: P1DN:CAA87345.1: GSPDB:GN00028: CESP:F15G9.4b

A;CROSS-REFERENCES: EMBL:Z47070; F
A:Experimental source: clone T09B9

A; Experiments:
C: Genetics:

C;Genetics:
A:Gene: him-4: F15G9.4b

A:Gene: HIM-4; F1:
A:Man position: x

A:Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
B;Exons: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 3033/3; 3033/3;
C;Exons: 4225/1; 4363/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/3;
D;Exons: 4225/1; 4363/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/3;

Query Match 7.2%: Score 196.5; DB 2; Length 5198;

Query Match Best Local Similarity

| | | |
|-----------------------|------------------|---|
| BEST LOCAL SIMILARITY | 28.4%; | FREQ. NO: 2.3E-03; |
| Matches | 88: Conservative | 42: Mismatches 138: Indels 65: Gaps 19: |

59 PTIVE-PHVTAV-WGKNVSLKCLIEVNETITOISWEKIHGKSSOTVAVHHPOYGFSVOGE 116

| | | | | | | |
|----|-----|-------------------------|--------------------|------------------------|-----------------|-----|
| QY | 59 | FLIVE-FVILAV | -WGNWWSUKCTVAVNEII | WISMENTKNSQQA | VAVHMFVIGISVQGE | 111 |
| | | | | | | |
| | | | | | | |
| Dp | 793 | PTTIESPHTVRVNIEROVTLOCL | -AVGIPPEIEKOK | ---GNVLLATLNNRYTLOADG- | 847 | |

117 YQGRVI.FKNYSI.NDATIT.IHNI.GFSDSGKYICKAVTFPI.GNAOSS"TT--VTVLVEPTVSL 174

QY II / IQGKVLFIKISLNLVAIIILHNIGFSDSGAKVLCNAVIFFLGNQAQSIII--VIVLVVERIVSN I77

D6 848 -----NLIITAAQI-----EDOGRTCIARN-TYGQOSOSTIMTGLVSLVGLGH 891

175 IKGPDSLDGCNETYAAICIAAATGKPVAHIDWEGDI.GEMESTTTSFPNETATTISOYKLF 234

| | | | |
|----|-----|---|-----|
| QY | 175 | IKRPSLLDGGNETVAAICLAAATGAFVAHIDWEGDUGEMESITTSFFNFETAILISQIKLF | 943 |
| D6 | 892 | VBBDFQVREGDITITIS--CWAACGMPKPSITVMIKKDKPVR-----GPTIKIEGGSLIL | 943 |

Q. 025 0006980B 01TC000000AL EMDTPVCEII - - - DIAVADE - - - VSIYTGVDGDNW- 380

| | | | | | | |
|----|-----|---|-------------------------|--------------|--------------|-----|
| QY | 235 | PREFARGR--- | RITCVKHPALEKDIRYSPIL--- | DIQYAPE----- | VSIVIGYDGNW- | 280 |
| Dh | 944 | RIEGBNPKDEGKYTCITAVSPAGNSTLHINVOLIKKEEFVYKPEGGIVFKETISGMDKXHV | 1003 | | | |

Q: 301 ----- EYCPKCYNI KONA DANBPBPCKSVSPIDGOWP----- DGLI ASDNTI HEVH 326

| | | |
|----|------|---|
| Qy | 281 | -----FVGRKGWLLXCNADANPPPPFKSVSRSLDQWP-----DGLLASSNTLHHFVH 328 |
| Dh | 1004 | AVVNSTHNVLDGEFAIPCVWSCTPPDDI-ITW-VINDGR-PITPNSRDFETVADNTL-IVR 10599 |

327 P I T E N Y S C I N V I C K Y T N S I G O R S D O K I V T Y S D V P 359

| | | | |
|----|------|------------------------------------|------|
| QY | 327 | PLTFNYSGVYICKVINSLGQRSDQKVYIYISDVP | 359 |
| | | : : : : | |
| pB | 1060 | KADKSYSGVYTCOATNSAGDNEOKTTIRIMNTP | 1092 |

Search completed: October 6, 2005, 10:21:09

search completed: October 1997
Job time : 17.7671 secs

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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:34:02 ; Search time 75.6517 Seconds
(without alignments)
3452.143 Million cell updates/sec

Title: US-09-972-268-10
Perfect score: 2711
Sequence: 1 MARTPGSPPLCPGGKAQLS.....KHQNNDPKRYVDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|---------------|---------------------|
| 1 | 2406 | 88.7 | 510 | 2 Q9JLB8 | Q9jlb8 mus muscu |
| 2 | 2125 | 78.4 | 438 | 2 Q9JLB7 | Q9jlb7 mus muscu |
| 3 | 1906.5 | 70.3 | 549 | 2 Q9NQ33 | Q9nq33 homo sapien |
| 4 | 1858 | 68.5 | 366 | 2 Q6NV23 | Q6nv23 homo sapien |
| 5 | 1837.5 | 67.8 | 549 | 2 Q9JLB9 | Q9jlb9 mus muscu |
| 6 | 1793.5 | 66.2 | 549 | 2 Q9D006 | Q9d006 mus muscu |
| 7 | 1235 | 45.6 | 267 | 2 Q8NC05 | Q8nc05 homo sapien |
| 8 | 1173.5 | 43.3 | 407 | 2 Q9Y412 | Q9y412 homo sapien |
| 9 | 648.5 | 23.9 | 304 | 2 Q9BVA9 | Q9bva9 homo sapien |
| 10 | 602 | 22.2 | 515 | 1 PVRL1 MOUSE | Q9jklf6 mus muscu |
| 11 | 598 | 22.1 | 515 | 2 Q6P9K9 | Q6p9m9 mus muscu |
| 12 | 589 | 21.7 | 515 | 1 PVRL1 PIG | Q9gl176 mus scrofa |
| 13 | 588 | 21.7 | 517 | 1 PVRL1 HUMAN | Q152233 homo sapien |
| 14 | 540 | 19.9 | 530 | 1 PVRL2 MOUSE | Q32507 mus muscu |
| 15 | 537 | 19.8 | 530 | 2 Q80X35 | Q80xj5 mus muscu |
| 16 | 534.5 | 19.7 | 295 | 2 Q9ERP5 | Q9erf5 mesocricetu |
| 17 | 528 | 19.5 | 298 | 2 Q9GL74 | Q9gl74 cercopithec |
| 18 | 527 | 19.4 | 538 | 1 PVRL2 HUMAN | Q92692 homo sapien |
| 19 | 526.5 | 19.4 | 295 | 2 Q9GL75 | Q9gl175 bos taurus |
| 20 | 523.5 | 19.3 | 510 | 2 Q96NY8 | Q96ny8 homo sapien |
| 21 | 522.5 | 19.3 | 510 | 2 Q96K15 | Q96k15 homo sapien |
| 22 | 511.5 | 18.9 | 483 | 2 Q9DBP8 | Q9dbp8 mus muscu |
| 23 | 503.5 | 18.6 | 464 | 2 Q8GL25 | Q8gl25 xenopus tro |
| 24 | 495 | 18.3 | 508 | 2 Q8CED8 | Q8ced8 mus muscu |
| 25 | 495 | 18.3 | 508 | 2 Q8R007 | Q8r007 mus muscu |
| 26 | 494 | 18.2 | 463 | 2 Q66J72 | Q66j72 xenopus lae |
| 27 | 467 | 17.2 | 467 | 2 Q8CF2 | Q8cf2 mus muscu |
| 28 | 467 | 17.2 | 467 | 2 Q91VT9 | Q91vt9 mus muscu |
| 29 | 427.5 | 15.8 | 449 | 2 Q9UE16 | Q9ue16 homo sapien |
| 30 | 418 | 15.4 | 417 | 1 PVRL2 CERAE | Q32506 cercopithec |
| 31 | 411.5 | 15.2 | 412 | 2 Q9R1E1 | Q9r1e1 rattus norv |

| | | | | | |
|----|-------|------|-----|-------------|--------------------|
| 32 | 407 | 15.0 | 400 | 2 Q8HY16 | Q8hy16 cebus apell |
| 33 | 406.5 | 15.0 | 412 | 2 Q83611 | Q83611 rattus norv |
| 34 | 405 | 14.9 | 417 | 1 PVR HUMAN | P15151 homo sapien |
| 35 | 402.5 | 14.8 | 408 | 2 Q91WP1 | Q91wp1 mus muscu |
| 36 | 400.5 | 14.8 | 408 | 2 Q8K094 | Q8k094 m hypotheri |
| 37 | 399.5 | 14.7 | 408 | 2 Q8BVF6 | Q8bvfe mus muscu |
| 38 | 395 | 14.6 | 401 | 2 Q08835 | Q08835 cercopithec |
| 39 | 390 | 14.4 | 403 | 2 Q8HY15 | Q8hy15 lemuz catta |
| 40 | 386 | 14.2 | 412 | 2 Q8HY14 | Q8hy14 oryctolagus |
| 41 | 355.5 | 13.1 | 415 | 2 Q60977 | Q60977 mus muscu |
| 42 | 326.5 | 12.0 | 416 | 2 Q7M048 | Q7m048 rattus norv |
| 43 | 309 | 11.4 | 417 | 2 Q7TNL1 | Q7tnl1 mus muscu |
| 44 | 305.5 | 11.3 | 442 | 2 Q9BY67 | Q9by67 homo sapien |
| 45 | 304.5 | 11.2 | 390 | 2 Q66KX2 | Q66kx2 xenopus lae |

ALIGNMENTS

| | | | | | |
|--|---|--|--------------|------|---------|
| RESULT 1 | | | | | |
| Q9JLB8 | ID | Q9JLB8 | PRELIMINARY; | PRT; | 510 AA. |
| AC | Q9JLB8; | | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | | | |
| DT | 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) | | | | |
| DE | Cell adhesion molecule nectin-3 beta. | | | | |
| GN | Name=Pvr13; | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291; | | | | |
| RA | SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M., | | | | |
| RA | Tachibana K., Mizoguchi A., Takai Y.; | | | | |
| RT | "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules that shows homophilic and heterophilic cell-cell adhesion activities." | | | | |
| RL | J. Biol. Chem. 275:10291-10299(2000). | | | | |
| DR | EMBL; AF195834; AAF63686.1; -. | | | | |
| DR | MGD; MGI:1930171; Pvr13. | | | | |
| DR | GO; GO:0005913; C:cell-cell adherens junction; IDA. | | | | |
| DR | GO; GO:0005615; C:extracellular space; TAS. | | | | |
| DR | GO; GO:0016021; C:integral to membrane; TAS. | | | | |
| DR | GO; GO:0005515; F:protein binding; IPI. | | | | |
| DR | GO; GO:0016337; P:cell-cell adhesion; IDA. | | | | |
| DR | InterPro; IPR003599; Ig. | | | | |
| DR | InterPro; IPR007110; Ig-like. | | | | |
| DR | Pfam; PF00047; ig; 1. | | | | |
| DR | SMART; SM00409; IG; 1. | | | | |
| DR | PROSITE; PS50835; IG LIKE; 3. | | | | |
| SQ | SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64; | | | | |
| Query Match 88.7%; Score 2406; DB 2; Length 510; | | | | | |
| Best Local Similarity 89.2%; Pred. No. 9.9e-173; | | | | | |
| Matches 456; Conservative 22; Mismatches 31; Indels 2; Gaps 2; | | | | | |
| Qy | 1 | MARTPGSPPLCPGGKAQLSSALLGALLLQPTPPPLLLLPPLLLFRRLCGALAGPI | 60 | | |
| Db | 1 | MARTPGPAPLCPGGKAQLSAPFAAGLLLPAPTTPPLLLLTPLLLFRRLCGALAGSI | 60 | | |
| Qy | 61 | IVPHVTVAVGKNSVKCLLEVNETTQISWEKHGSSQTVAVHHPOYGFSGVQYQGR | 120 | | |
| Db | 61 | IVPHVTVAVGKNSVKCLLEVNETTQISWEKHGSSQTVAVHHPOYGFSGVQYQGR | 120 | | |
| Qy | 121 | VLFKNYSINDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTTLVLTVEPVSILKGPDS | 180 | | |
| Db | 121 | VLFKNYSINDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTTLVLTVEPVSILKGPDS | 180 | | |
| Qy | 181 | LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATISQYKLPFTTSPAR | 240 | | |
| Db | 181 | LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATISQYKLPFTTSPAR | 240 | | |

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Db 181 LIDGNETVAACVAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLPPTRFAR 240
Qy 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPF 300
Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTNYSGVYICKVTNSLQORSQDKVIYISDVPP 360
Db 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTNYSGVYICKVTNSLQORSQDKVIYISDIPL 360
Qy 361 KOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPYSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPYSYLDKVIDLPPTHKPPPLYEERI 420
Qy 421 PPLPOKDLF-OPEHLPLQTOFKEREVGNLOHNSGLNRSFDYEDENPVGEGDQOQVPLY 479
Db 421 PSLPOKDLGQTEHLPLQTOFKKEGAGGLQPSNGPISRRFDYEDSTMQEDGTQRMCPY 480
Qy 480 NMCYQDRSPGKHONNDPKRVYIDPREHYV 510
Db 481 SQMCHQDRSPRQHPRN-PERLYINPREHYV 510

RESULT 2
Q9JLB7
ID Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2029403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3, a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299 (2000).
DR EMBL; AF1930171; Pvr13.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 438 AA; 47361 MW; 2A0A44165B02FEF CRC64;

Query Match 78.4%; Score 2125; DB 2; Length 438;
Best Local Similarity 93.7%; Pred. No. 1.2e-151;
Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MARTPGSPLCGCGKAQLSSASLLGALLLQPTPTPPPLLLLPFLFRLCGALAGPI 60
Db 1 MARTPGAPLCPGCGKAQLSSAFPPAAGLLLPAPTPPPPLLLLPFLFRLCGALAGSI 60
Qy 61 IVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHQYGSVQGEYQGR 120
Db 61 IVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHQYGSVQGEYQGR 120
Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTVLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTVLVEPTVSLIKGPD 180
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Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTVLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLPPTRFAR 240
Db 181 LIDGNETVAACIAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLPPTRFAR 240
Qy 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPF 300
Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTNYSGVYICKVTNSLQORSQDKVIYISDVPP 360
Db 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTNYSGVYICKVTNSLQORSQDKVIYISDIPL 360
Qy 361 KOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPYSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPYSYLDKVIDLPPTHKPPPLYEERI 420
Qy 421 PPLPOKDL 428
Db 421 PSLPOKDL 428

RESULT 3
Q9NQ33
ID Q9NQ33 PRELIMINARY; PRT; 549 AA.
AC Q9NQ33;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AP282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 70.3%; Score 1906.5; DB 2; Length 549;
Best Local Similarity 67.8%; Pred. No. 4.9e-135;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;

Qy 1 MARTPGSPLCGCGKAQLSSASLLGALLLQPTPTPPPLLLLPFLFRLCGALAGPI 60
Db 1 MARTLPSPLCPGCGKAQLSSASLLGALLLQPTPTPPPLLLLPFLFRLCGALAGPI 60
Qy 61 IVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHQYGSVQGEYQGR 120
Db 61 IVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHQYGSVQGEYQGR 120
Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTVLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTVLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLPPTRFAR 240
Db 181 LIDGNETVAACIAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLPPTRFAR 240
Qy 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPF 300
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Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIYISDVP- 359
Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIYISDPT 360
Qy 360 -----PKQTSIAVAGAVICAVLALFTIA 383
Db 361 TTTTLOPTQIOWHPSTADIEDLATEPKLPFPPLSTLATIKODDIIATIIASVUGALFVLVS 420
Qy 384 IFVTVLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424
Db 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQDELDSYVDSVKENKNPV- 478
Qy 425 QKDLFOPEHL--PLQTFQKEREVGNLQHSNGLSRSPDYEDNPVGDGICQOMPLYNQM 482
Db 479 -NNLIRKDYLEPEKTQW-----NNVENLNRP-ERPMDYYEDLXMGKMFVSD----- 523
Qy 483 CYQDRSPGKHONNDPKRV-----YIDPREHYV 510
Db 524 -----EHYDENEDDLVSHVDGVSISRREYV 549

RESULT 4
Q6NVZ3 PRELIMINARY; PRT; 366 AA.
AC Q6NVZ3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE VRL3 protein.
GN Name=VRL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC067808; AAH67808.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 3.
SQ SEQUENCE 366 AA; 39722 MW; 591D0A4687C30BA CRC64;

Query Match 68.5%; Score 1858; DB 2; Length 366;
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Best Local Similarity 99.2%; Pred. No. 1.3e-131;
Matches 353; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLFSLRCGALAGPI 60
Db 1 MARTLRSPPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLFSLRCGALAGPI 60
Qy 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVOGEYQGR 120
Db 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVOGEYQGR 120
Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSPFNETATITISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSPFNETATITISQYKLPFTRFAR 240
Qy 241 GRRITCVVKGPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVKGPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIYIS 356
Db 301 KSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIYIS 356

RESULT 5
Q9JUB9 PRELIMINARY; PRT; 549 AA.
AC Q9JUB9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3, a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
RL EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60582 MW; 5492C9ABB472F185 CRC64;

Query Match 67.8%; Score 1837.5; DB 2; Length 549;
Best Local Similarity 68.6%; Pred. No. 7.8e-130;
Matches 371; Conservative 35; Mismatches 58; Indels 77; Gaps 9;
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Qy 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLFSLRCGALAGPI 60
Db 1 MARTPGAPLCPGGKQAQLSSAFPPAAGLLLPATPPPLLLLPFLLSRLCAGLAGSI 60
Qy 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVOGEYQGR 120
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Db 61 IVEPHVTAVGKNSVLSKCLIEVNETTQISWEKHGKSTQTVAVHHPQYGFSGYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVVLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVVLVEPTVSLIKGPD 180
Qy 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRITTCVVKHPALEKDIRYFILDIOYAPVSVTVGDGNFVGRKGVNLKCNADANPPPF 300
Db 241 GRITTCVVKHPALEKDIRYFILDIOYAPVSVTVGDGNFVGRKGVNLKCNADANPPPF 300
Qy 301 KSVMSRLDGPWPGLLASDNLTHFVHPLTFNYSGVYCKVTNSLQSRSDQKVYIISDVPF 360
Db 301 KSVMSRLDGPWPGLLASDNLTHFVHPLTFNYSGVYCKVTNSLQSRSDQKVYIISDVPF 360
Qy 361 KQT-----SSIA-----VAGAVIGAVIALFIIA 383
Db 361 TTTLOPTVQWSSPADVQDIATEHKKLPPLSTLTKDPTIGTIIASVVGGAFLVLVS 420
Qy 384 IFVTLLTPRKR-----PSYLDKVIDLPPTHK-----PPPLYEERSPELPQ 425
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPSDMQESQIDVLHODELSDYPSVKKNKPNV-- 478
Qy 426 KDLFQPEHL--PLQTFKEREVGNLQHSNGLSRSDYEDENPVG-----EDG 471
Db 479 NNLRKDYLEEPEKTQW--NNVENLTFF----ERPMYDYLKMGKMFVSERYNESDG 532
Qy 472 I 472
Db 533 L 533

RESULT 6
Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610301B19 product:poliovirus receptor-related
DE 3, full insert sequence.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=9229253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

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RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Fujimoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Adakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanaokani T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ RECEPTOR.
Qy SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

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Query Match 66.2%; Score 1793.5; DB 2; Length 549;
Best Local Similarity 67.1%; Pred. No. 1.6e-126;
Matches 363; Conservative 38; Mismatches 63; Indels 77; Gaps 9;
Qy 1 MARTPGPPLCPGCGKQAQSSALLGAGLLQLPPTPPPLLLLPPLLPRLCGALAGPI 60
Db 1 MARTPGPPLCPGCGKQAQSSALLGAGLLQLPPTPPPLLLLPPLLPRLCGALAGSI 60
Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETTQISWEKHGKSTQTVAVHHPQYGFSGYQGR 120
Db 61 IVEPHVTAVGKNSVLSKCLIEVNETTQISWEKHGKSTQTVAVHHPQYGFSGYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVVLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVVLVEPTVSLIKGPD 180
Qy 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 SIDGGNETVAACVCSGTGKPVQIDWEGDLGEREFSTISFLNETATIVSQYELFPTFRAR 240

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Qy 241 GRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGKGVNLCNADANPPPF 300
Db 241 GRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGKGVNLCNADANPPPF 300
Qy 301 KSVMSRLDGGWPDPGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVVF 360
Db 301 KSVMSRLDGGWPDPGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVVF 360
Qy 361 KQT-----SSIA-----VAGAVIGAVIALFIIA 383
Db 361 TTTILQPTVQWSSPADVQDIATEHKLPPLSLTLATLKDDTIGTIIASVVGALFLVLVS 420
Qy 384 IFVTVLTPKRR-----PSYLDKVIDLPPTHK-----PPPLYEERSPPLPQ 425
Db 421 ILAGVFCVRRRTFRGDFYAKNYIPPSDMQKESQIDVLHQDELSDYPSVKKNPNV-- 478
Qy 426 KDLFQPEHL--PLOTQFKEREVGNLQHSNGLNSRSDYEDENPVG-----EDG 471
Db 479 NNLRKYOLEEPEKTQW--NNVENLTRP----ERPMDYEDLKMGMKFSVDERYNESEDG 532
Qy 472 I 472
Db 533 L 533

RESULT 7
Q8NC05
ID Q8NC05 PRELIMINARY; PRT; 267 AA.
AC Q8NC05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; --
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 45.6%; Score 1235; DB 2; Length 267;
Best Local Similarity 96.0%; Pred. No. 7.6e-85;
Matches 242; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 41 LLLPFL--LFSRLCGALAGPIIIEPHVTAVWGNVSLKLIENETITQISWEKIHGKS 98
Db 16 LLRGPLLPRFSFGNPRALAGPIIIEPHVTAVWGNVSLKLIENETITQISWEKIHGKS 75
Qy 99 SQTAVHHPOYGFSGVQGRVLPKNYSNDATITLHNIGFSDSGKYICAKVTFPLGNA 158
Db 76 SQTAVHHPOYGFSGVQGRVLPKNYSNDATITLHNIGFSDSGKYICAKVTFPLGNA 135
Qy 159 QSSSTTVTLVPTVSLIKGPSLIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTT 218
Db 136 QSSSTTVTLVPTVSLIKGPSLIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTT 195
Qy 219 SFPNETATIIISQYKLPFRFARGRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYD 278
Db 219 SFPNETATIIISQYKLPFRFARGRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYD 278
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Db 196 SFPNETATIIISQYKLPFRFARGRRITCVVKKPALEKDIRYSFILDIOYAPEVSVTGYD 255
Qy 279 NWFVGRKGVNLK 290
Db 256 NWFVGRKGVNLK 267

RESULT 8
Q9Y412
ID Q9Y412 PRELIMINARY; PRT; 407 AA.
AC Q9Y412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Hypothetical protein DKFZP566B0846 (fragment).
GN Name=DKFZP566B0846;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Otterwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 407 AA; 45718 MW; 45B6C05068D63AC CRC64;

Query Match 43.3%; Score 1173.5; DB 2; Length 407;
Best Local Similarity 62.8%; Pred. No. 5.8e-80;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Qy 143 SGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPSLIDGGNETVAAICIAATGKPA 202
Db 1 SGKYICKAVTFPLGNAQSSTTVTLVPTVSLIKGPSLIDGGNETVAAICIAATGKPA 60
Qy 203 HIDWEGDLGEMESTTTSPFNETATIIISQYKLPFRFARGRRITCVVKKPALEKDIRYSFI 262
Db 61 HIDWEGDLGEMESTTTSPFNETATIIISQYKLPFRFARGRRITCVVKKPALEKDIRYSFI 120
Qy 263 LDIOYAPEVSVTGYDGNWFGKGVNLCNADANPPPFKSVMSRLDGGWPDPGLASDNTL 322
Db 121 LDIOYAPEVSVTGYDGNWFGKGVNLCNADANPPPFKSVMSRLDGGWPDPGLASDNTL 180
Qy 323 HFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP----- 359
Db 181 HFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP----- 240
Qy 360 -----FKOTSSIAVAGAVIGAVIALFIIAFTVLLTPRK--RPSYLDKV 403
Db 241 EPKPLPPLSTLTIKDDTIATIIASVVGALFLVSVLAGIFCYRRRTFRGDFYAKN 300
Qy 404 IDLPPH-----KPPLYEERSPPLPQKDLFQPEHL--PLOTQFKEREV 446
Db 301 Y-IPSDMQKESQIDVLQDELDPYPSVKKNPNVNNLRKYOLEEPEKTQW-----N 354
Qy 447 NLQHSNGLNSRSDYEDENPVG 468
Db 355 NVENLNR-ERPMDYEDLKM 375

RESULT 9
Q9BVA9
ID Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Hypothetical protein DKFZP566B0846 (fragment).
GN Name=DKFZP566B0846;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Otterwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 407 AA; 45718 MW; 45B6C05068D63AC CRC64;
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Db 44 GTDVVLHCSFANPLPSVKITQVWQKASNGSKQWAIYNTMGVSVLPYPPEKRVFELRPS 103
Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEVTSLIKGPDSLDG--- 184
Db 104 FIDGTIRLSGLEDEDEGMYCEPATFTPTGNRESQNLNTVMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAACIAATGKPAHIDWEGDL-GEMESTTTFPNETATIIISQYKLPFRFARGR 242
Db 163 QDNKVLVATCTSANGKPPSAVSWETRLKGEAEYQEIIRNPNGTIVTVISRYRLVPSREAHQ 222
Qy 243 RITCVVKHPALEKDIRYFSLDIOYAPEVSVTGDGNWFGVGRKGNLKNADANPPPPFKS 302
Db 223 SLACIVNY-HLDR-FRESLTINVQYEPVETIEGFGNWLQRTDVKLTCKADANPPATEY 280
Qy 303 VWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTSNLGORSQDKYIYISDVFPKQ 362
Db 281 HWTTLNGLPKGVEAQNRTLFFRGFTYSLAGTICEATNPIGTRSGQVEVNIETFPYTP 340
Qy 363 TSS-----IAVAGAVIGAVLAFIIFVTVLLTPRKK--RPSYLDK----- 402
Db 341 TPEHRRAGQMPATIIIGVAGSVLLVIVGGIIVALLRRRHHTFKGDYSTKKHYNGYS 400
Qy 414 PLYEERSPPLPKDLFQ-----PEHLPLQTOFKEREVGNLQH-----SNGLNS 456
Db 385 -----KGYSTKKHYNGYSKAGIQHPHMAQ-----NLQTPDSDDEKKASPLGG 432
Qy 457 RSPFYEDENPVGEDIGIQM-----YPLYN-----QMCYQDRSPGKHQWND 497
Db 433 SSYEEREEGGGGERKVGKPPKPYDEDAKRPYFTVDEAEARQDGYGDRTLGYQY---D 489
Qy 498 PKRV-----YIDPREHYV 510
Db 490 PEQLDLAENMVSONDGSFISKWEYV 515

RESULT 11
Q6P9M9 PRELIMINARY; PRT; 515 AA.
AC Q6P9M9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Poliovirus receptor-related 1.
GN Name=Prv1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
```

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL EMBL; BC060694; AH60694.1;
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG2; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Receptor.
SQ SEQUENCE 515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;

Query Match 22.1%; Score 598; DB 2; Length 515;
Best Local Similarity 31.08; Pred. No. 1.9e-36;
Matches 155; Conservative 86; Mismatches 171; Indels 88; Gaps 16;

Qy 71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGYQGRVLFKNYS 127
Db 44 GTDVVLHCSFANPLPSVKITQVWQKASNGSKQWAIYNTMGVSVLPYPPEKRVFELRPS 103
Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEVTSLIKGPDSLDG--- 184
Db 104 FIDGTIRLSGLEDEDEGMYCEPATFTPTGNRESQNLNTVMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAACIAATGKPAHIDWEGDL-GEMESTTTFPNETATIIISQYKLPFRFARGR 242
Db 163 QDNKVLVATCTSANGKPPSAVSWETRLKGEAEYQEIIRNPNGTIVTVISRYRLVPSREAHQ 222
Qy 243 RITCVVKHPALEKDIRYFSLDIOYAPEVSVTGDGNWFGVGRKGNLKNADANPPPPFKS 302
Db 223 SLACIVNY-HLDR-FRESLTINVQYEPVETIEGFGNWLQRTDVKLTCKADANPPATEY 280
Qy 303 VWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTSNLGORSQDKYIYISDVFPKQ 362
Db 281 HWTTLNGLPKGVEAQNRTLFFRGFTYSLAGTICEATNPIGTRSGQVEVNIETFPYTP 340
Qy 363 TSS-----IAVAGAVIGAVLAFIIFVTVLLTPRKK--RPSYLDK----- 402
Db 341 TPEHRRAGQMPATIIIGVAGSVLLVIVGGIIVALLRRRHHTFKGDYSTKKHYNGYS 400
Qy 403 VIDLPPTHKPPPLYEERSPPLPKDLFQPEHLPLQTOFKEREVGNLQHSNLSRSDYE 462
Db 401 KAGIQPHI--PPMAQNLQYPPDSDD-----EKKAGPLGSS-----SYEE 438
Qy 463 DENPVGSDGTQM---YPLYN-----QMCYQDRSPGKHQWNDPKRV-- 501
Db 439 EEEEGGGGGERKVGKPPKPYDEDAKRPYFTVDEAEARQDGYGDRTLGYQY---DPEQLDL 495
Qy 502 -----YIDPREHYV 510
Db 496 AENMVSONDGSFISKWEYV 515

RESULT 12
PRV1_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (Hvnc) (Nectin 1).
GN Name=PRV1; Synonyms=HVCE, PR1;
```

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OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
CC -!- FUNCTION: Probably involved in cell adhesion. Receptor for
CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
CC cells.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF308632; AAC30281.1; -.
DR HSSP; Q05793; IGL4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
SQ SEQUENCE 515 AA; 57047 MW; BPAB00320DDE3785 CRC64;

Query Match 21.78; Score 589; DB 1; Length 515;
Best Local Similarity 30.28; Pred. No. 9.1e-36;
Matches 156; Conservative 83; Mismatches 194; Indels 84; Gaps 15;

QY 52 LCGALQPIIVEPHVTAWGKNVSKLIE---VNETITQISWEKIHGKSQTVAVHPQ 108
DB 25 LPGAHTQVQVNDMSYGFIDGVDVLHCSFANPLPGVKITQVTWQATNGSKQNVAINPA 84

QY 109 YGFSVQGEYQGRVLFRNYSLNDATITLHNTGFSQGYKICAVTFFPLGNAQSSTTVLV 168
DB 85 MGVSVLAPYRERFELRPSFTDGTIRLSRLEDEGYVICFATFFPAGNRESQNLTVMA 144

QY 169 EPTVSLIKGPDSLIDG---GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPNE 223
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Db 145 KPT-NWIEGTAQVLRRAKKGDKDVLVATCTSANGKPPSVVSWETHLKGEAEYQIRPNPG 203
QY 224 TATIIISOYKLPFRFARGRRITCVVXHPALEKDIRYSFILDIOYAPVSVSTGDNWFGV 283
DB 204 TTVVISRYLRVPSREDHROSACLACIVNYHM--DRFRESLTINQYEPVETIEGFDGNWYLQ 261
QY 284 RKGVLNLCNADANPPFPKFSVWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNS 343
DB 262 RMDVKLTCADANPPATEYVHTWTLNGLPKGVQAQRNLTFRGPINYSMAGTYICEATNP 321
QY 344 LQGRSDQKVIYISDVPFKQTS-----SIAVAGAVIGAV-LALFIIAIFVTVLLTP 392
DB 322 IGRSQQVEWITEFPVTPSPPEHRRAGQVPTAIIIGVVGSILLVLVVGGIIVVALCRR 381
QY 393 RKK-RSYLDK-----VIDLPPTHKPPPIYEERSPLPKQDLFQPEHLPLQTFKE 442
DB 382 RHTFKGDYSTKHHVYNGXSKAGIPQHH--PPMAQNQLQYPEDSD--E 425
QY 443 REVGNLQHSNLSRSDYEDENPVGEDGIGQMVPLYN-----QMCYQD 486
DB 426 KKAQPL-----GSSSYEEEBEGGGERKVGPHPKYDEDAKRPYFTVDEABARQDGYGD 481
QY 487 RSPGKHQNDPKRV-----YIDPREHYV 510
DB 482 RTLGYQY---DPQLDLAENMVSNQDGSFISKKEWYV 515

RESULT 13
PVRI_HUMAN STANDARD; PRT; 517 AA.
AC Q1523; Q75465; Q9HBE6; Q9HEW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD111 antigen).
DE Name=PVRL1; Synonyms=HVEC, PRR1;
DE OS Homo sapiens (Human).
DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
DE OX NCBI_TaxID=9606;
DE RN [1]
DE RP SEQUENCE FROM N.A. (ISOFORM DELTA).
DE RX MEDLINE=95237621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G;
DE RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
DE RA Dubreuil P.;
DE RT "cDNA characterization and chromosomal localization of a gene related
DE to the poliovirus receptor gene.";
DE RL Gene 155:261-265(1995).
DE RN [2]
DE RP SEQUENCE FROM N.A. (ISOFORM DELTA).
DE RX MEDLINE=98279152; PubMed=9616127; DOI=10.1126/science.280.5369.1618;
DE RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
DE RA Spear P.G.;
DE RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
DE protein 1 and poliovirus receptor.";
DE RL Science 280:1618-1620(1998).
DE RN [3]
DE RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
DE RX MEDLINE=21256041; PubMed=11356977;
DE RX DOI=10.1128/JVI.75.12.5684-5691.2001;
DE RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
DE RA Campadelli-Fiume G., Dubreuil P.;
DE RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
DE nectin1 (or prrl-HIGR-Hvec) modulates positively and negatively
DE susceptibility to hsv infection.";
DE RL J. Virol. 75:5684-5691(2001).
DE RN [4]
DE RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
DE RX MEDLINE=20392396; PubMed=10932188; DOI=10.1038/78119;
DE RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
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RESULT 14
PVR2_MOUSE STANDARD; PRT; 530 AA.
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 08-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (HvEB) (Nectin 2) (Poliovirus receptor homolog).
GN Names=Pvr12; Synonyms=Mph, Pvr, Pvs;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RP MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene.";
RL J. Virol. 66:2807-2813(1992).
RN [2]
SEQUENCE FROM N.A. (ISOFORM BETA).
RP STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94117928; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus.";
RL J. Biol. Chem. 269:8431-8438(1994).
RN [3]
SEQUENCE FROM N.A. (ISOFORM BETA).
RP STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
CHARACTERIZATION.
RP MEDLINE=99214397; PubMed=10196354;
RX Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RA "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)
RA mediates entry of pseudorabies virus but not herpes simplex virus
RA types 1 and 2.";
RL J. Virol. 73:4493-4497(1999).
CC -1- FUNCTION: Receptor for alphaherpesvirus (such as murine HSV) entry
CC into cells.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC -1- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.

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CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M80206; AAA39734.1; -.
DR EMBL; D26107; BAA05103.1; -.
DR EMBL; BC059941; AAH59941.1; -.
DR PIR; A38211; HLMSE3.
DR PIR; A53437; A53437.
DR MGD; MGI:97822; Pvr12.
DR InterPro; IPR007110; Ig-Like.
DR Pfam; PF00047; Ig_3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 31 Potential.
FT CHAIN 32 530 Poliovirus receptor related protein 2.
FT DOMAIN 32 351 Extracellular (Potential).
FT TRANSMEM 352 372 Potential.
FT DOMAIN 373 530 Cytoplasmic (Potential).
FT DOMAIN 32 147 Ig-like V-type.
FT DOMAIN 153 247 Ig-like C2-type 1.
FT DOMAIN 252 337 Ig-like C2-type 2.
FT DISULFID 54 131 By similarity.
FT DISULFID 174 229 By similarity.
FT DISULFID 274 320 By similarity.
FT CARBOHYD 128 128 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 315 315 N-linked (GlcNAc...) (Potential).
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SEHPVKTFYFQVSCADEMPRYHELPTLEERSGFLG
ATGLGP -> DTPQASRDVPLVGVGTLVLLAGGLG
ALILLGRRRRKSPGGGNDGRGSDYDPTQVFGNGPWFV
RSASPMPMPDGRDEEEEEEKABEGLMPPHESPKDDM
ESHLGSLISRAVYV (in isoform Alpha).
/FTId=VSP_002630.
/FTId=VSP_002631.
FT VARSPIC 468 530 Missing (in isoform Alpha).
FT SEQUENCE 530 AA; 57317 MW; 0ED71BFA2B231BBE CRC64;
SQ
Query Match 19.9%; Score 540; DB 1; Length 530;
Best Local Similarity 28.8%; Pred. No. 4.7e-32; Indels 80; Gaps 17;
Matches 153; Conservative 85; Mismatches 214;
QY 30 LLOQPTPPPLLLPPLLLFSLRCGALAGPIIYEPHVTAVMGKNVSLKC--LIEVNETIT 87
Db 6 VLPPSRSLPTLLPLLLLLQLQETGAQDVVRVLPVVRGRLGTVLPCHLLPTTERVS 65
QY 88 QISWEKHGKSSOTVAHHHPQYGFVSQGEY--QGRVLF-----KNVSLNDATITLHNIG 139
Db 66 QVTWQRLDG---TWAAAFHPSPGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRLGR 122
QY 140 FSDSGKVIKAVTFPLGNAQSSTTVTLVEP-----TVSLIKGPDLSLDGNETVAIICI 194
Db 123 VEDEGNTCEFAFPNGTRRGVTLVRIQAPENHAEQAQEVIIQPSV-----AVARCV 175
QY 195 AATGKPVAHIDWEGDLGEMESTTSPFN---ETATIIISOYKLPFPFARGRTTCVVKHP 251
Db 176 STGCRPPARITWISSLGG-EAKDTQEGIQAGVTIISRYSLVPVGRADGVKTCRVEHE 234
QY 252 ALEKDRYSFILDIQVAPEVSVTVGQCNWFWVGKGNLKNADANPPPFKSVWSRLDGQW 311
Db 235 SFPEPILLPVTLSVRYPPPEVSIISGYDDNMYLIGSEALITCDVRSNPEFTDYDSTTSGVF 294
QY 312 PDGLLASDNTLHFVHPLTFNYSGVWICKVTNSLQSRSDQKVIYSIDVPFPKQTSIAVAGA 371

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Db 295 PASAVAQSQL-LVHSDVRMNTTFCITATNAVGTGRAQVILVRESP--STAGAGATGG 351
Qy 372 VIGAVLALFI-IAIFVTVLTPRKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL 423
Db 352 IIGGIIAAIATAVAGTGILICROQRKEORLQAADBEELGPPSYKPTTAKALEBPEM 411
Qy 424 POK--DLFQPEHLPLQTF-----KEREVGNLQHSNGLN----- 455
Db 412 PSQFLTGASEHSPVKTPYFDAGVSCADQEMPRVHELPTLEERSGPLLGGATGSPSLV 471
Qy 456 -----SRSPDYEDENPVGSDGIQOMPLYNQMCYQDRSPGKHQND 497
Db 472 PPGNNVEGVSLSLEDEDEDEDFLDKINPIYDALSYP--SPSDSYQSKD 521

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RESULT 15

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Q80XJ5 ID Q80XJ5 PRELIMINARY; PRT; 530 AA.
AC Q80XJ5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Poliovirus receptor-related 2.
GN Name=Pvrl2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046770; AAH46770.1; -.
DR MGD; MGI:97822; Pvrl2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 530 AA; 57347 MW; 7ED1ABFA2F764ABA CRC64;

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Query Match 19.8%; Score 537; DB 2; Length 530;
 Best Local Similarity 28.6%; Pred. No. 7.8e-32;

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Matches 152; Conservative 87; Mismatches 213; Indels 80; Gaps 18;
Qy 30 LLOPPTPPPLLLPPLLSRLCGALAGPIIVPEPHVTAVGKNVSKC--LIEVNETIT 87
Db 6 VLPSPRLSPTLPLPLLLLLLLQETGAQDVRVRVLPEVGRGLGTVLPCHELLPTTTRVS 65
Qy 88 QISWEKTHGSSQTVAVHHPQYGFSGVGEY--QGRVLV-----KNYSLNDATITLHNIG 139
Db 66 QVTWORLDG---TVAAAFHFSFGVDPFNSQFSKORLSFVRARPTNADLRDATLAFRLR 122
Qy 140 FDSGKYICKAVTPPLGNAQSSSTTVTLVVP-----TVSLIKGPDLSIDGNETVAAICI 194
Db 123 VEDEGNYTCFAUFPNGTTRRGVTLWRVIAQPENHAEAEQVETIGQSV-----AVARCV 175
Qy 195 AATGKPVAHIDWEGDLGEMESTTTSFEN---ETATIIISOYKLFTRFARGRIITCVKHP 251
Db 176 STGGRPPARITWISSLGG-EAKDTQEPGIAQGTVTIIISRYSLVPVGRADGVKVTCTVEHE 234
Qy 252 ALEKDIRYSFILDIOVAPEVSVTGYDGNWFVGRGVNLKNADANPPFPKSVWSRLDQW 311
Db 235 SFEEPIILLPVTLSVRYPPESISGYDDNWLGRSEAILTCDVRNPEPTDYDWTTSGVF 294
Qy 312 PDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDVFPFKQTSIAVAGA 371
Db 295 PASAVAQSQL-LVHSDVRMNTTFCITATNAVGTGRAEQVILVRESP--STAGAGATGG 351
Qy 372 VIGAVLALFI-IAIFVTVLTPRKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPL 423
Db 352 IIGGIIAAIATAVAGTGILICROQRKEORLQAADBEELGPPSYKPTTAKALEBPEM 411
Qy 424 POK--DLFQPEHLPLQTF-----KEREVGNLQHSNGLN----- 455
Db 412 PSQFLTGASEHSPVKTPYFDAGVSCADQEMPRVHELPTLEERSGPLLGGATGSPSLV 471
Qy 456 -----SRSPDYEDENPVGSDGIQOMPLYNQMCYQDRSPGKHQND 497
Db 472 PPGNNVEGVSLSLEDEDEDEDFLDKINPIYDALSYP--SPSDSYQSKD 521

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Job time : 77.6517 secs

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11/14/2015 07:28:19 PM

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 21.3581 Seconds
(without alignments)
1782.508 Million cell updates/sec

Title: US-09-972-268-10
Perfect score: 2711
Sequence: 1 MARTPGSPICPGGKAQLS.....KHQNDPKRVYIDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 588 | 21.7 | 514 | 4 | US-09-949-016-11380 |
| 2 | 588 | 21.7 | 517 | 4 | US-09-723-368-4 |
| 3 | 584.5 | 21.6 | 458 | 4 | US-09-435-956A-1 |
| 4 | 565.5 | 20.9 | 518 | 4 | US-09-919-172-20 |
| 5 | 467.5 | 17.2 | 522 | 4 | US-09-949-016-7563 |
| 6 | 458.5 | 16.9 | 479 | 4 | US-09-723-368-2 |
| 7 | 458.5 | 16.9 | 479 | 4 | US-09-949-016-6278 |
| 8 | 409 | 15.1 | 456 | 4 | US-09-949-016-7564 |
| 9 | 402 | 14.8 | 417 | 4 | US-09-949-016-6729 |
| 10 | 400.5 | 14.8 | 408 | 3 | US-09-724-864-62 |
| 11 | 306.5 | 11.3 | 442 | 4 | US-09-778-510-20 |
| 12 | 306.5 | 11.3 | 442 | 4 | US-09-930-803-1 |
| 13 | 304.5 | 11.2 | 440 | 4 | US-09-866-028-61 |
| 14 | 304.5 | 11.2 | 440 | 4 | US-09-944-457-61 |
| 15 | 230.5 | 10.7 | 423 | 4 | US-09-778-510-22 |
| 16 | 235.5 | 9.4 | 398 | 4 | US-09-778-510-4 |
| 17 | 248.5 | 9.2 | 398 | 4 | US-09-778-510-6 |
| 18 | 248.5 | 9.2 | 398 | 4 | US-09-907-794A-84 |
| 19 | 248.5 | 9.2 | 398 | 4 | US-09-905-125A-84 |
| 20 | 248.5 | 9.2 | 398 | 4 | US-09-902-775A-84 |
| 21 | 248.5 | 9.2 | 398 | 4 | US-09-906-700-84 |
| 22 | 248.5 | 9.2 | 398 | 4 | US-09-903-603A-84 |
| 23 | 248.5 | 9.2 | 398 | 4 | US-09-904-920A-84 |
| 24 | 248.5 | 9.2 | 398 | 4 | US-09-909-064-84 |
| 25 | 248.5 | 9.2 | 398 | 4 | US-09-905-381A-84 |
| 26 | 248.5 | 9.2 | 398 | 4 | US-09-906-618-84 |
| 27 | 244.5 | 9.0 | 444 | 2 | US-08-659-984A-5 |

| | | | | | | |
|----|-------|-----|------|---|---------------------|-------------------|
| 28 | 244.5 | 9.0 | 444 | 3 | US-08-660-531-5 | Sequence 5, Appli |
| 29 | 238.5 | 8.8 | 432 | 4 | US-09-778-510-2 | Sequence 2, Appli |
| 30 | 237 | 8.7 | 421 | 2 | US-08-659-984A-1 | Sequence 1, Appli |
| 31 | 237 | 8.7 | 421 | 3 | US-08-660-531-1 | Sequence 1, Appli |
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| 33 | 199 | 7.3 | 1101 | 3 | US-08-986-485-2 | Sequence 2, Appli |
| 34 | 190.5 | 7.0 | 227 | 4 | US-09-205-258-947 | Sequence 947, App |
| 35 | 187.5 | 6.9 | 274 | 3 | US-09-570-367C-19 | Sequence 19, Appl |
| 36 | 187.5 | 6.9 | 274 | 4 | US-09-915-524-19 | Sequence 19, Appl |
| 37 | 187.5 | 6.9 | 274 | 4 | US-09-934-634-19 | Sequence 19, Appl |
| 38 | 178.5 | 6.6 | 467 | 3 | US-09-046-736-2 | Sequence 2, Appli |
| 39 | 177 | 6.5 | 626 | 4 | US-09-949-016-6213 | Sequence 6213, Ap |
| 40 | 177 | 6.5 | 664 | 4 | US-09-949-016-7850 | Sequence 7850, Ap |
| 41 | 175 | 6.5 | 887 | 3 | US-09-175-928-2 | Sequence 2, Appli |
| 42 | 175 | 6.5 | 887 | 4 | US-09-949-016-11044 | Sequence 11044, A |
| 43 | 175 | 6.5 | 837 | 4 | US-09-949-016-6515 | Sequence 6515, Ap |
| 44 | 174 | 6.4 | 511 | 4 | US-09-949-016-10054 | Sequence 10054, A |
| 45 | 174 | 6.4 | 1091 | 3 | US-08-986-485-5 | Sequence 5, Appli |

ALIGNMENTS

RESULT 1

US-09-949-016-11380
; Sequence 11380, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11380
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11380

Query Match 21.7%; Score 588; DB 4; Length 514;
Best Local Similarity 30.1%; Pred. No. 1.3e-46;
Matches 151; Conservative 85; Mismatches 176; Indels 90; Gaps 15;

| | | | |
|----|-----|--|-----|
| Qy | 71 | GKNSLKLCLIE---VNETITQISWEKIHGSSQTVAHHPOYGFSGVQYGRVLEKNYS | 127 |
| Db | 41 | GTDVVLHCSFANFLPSVKITQVTWQKSTNGSKONVALNPFMSGVSLAPRVERFEFLRPS | 100 |
| Qy | 128 | LNDAITITLHNIGSDSGYICKAVTFPLGNAQSTTTVLVEPTVLSLIGKPDLSLDG--- | 184 |
| Db | 101 | FTDGTIRLSLELEDEGVYICEFATFTGNREQLNLTVMKPTI-NWIEGTQAVLRAKKG | 159 |
| Qy | 185 | -GNETVAACIAATGKPEVAHIDWEGDL-GENESTTTSFPNETATIIISQYKLFPTFRFARGR | 242 |
| Db | 160 | QDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQIEIRNPNGTIVTISRVLVPSREAHQ | 219 |
| Qy | 243 | RITCVKHPALEKDIRYSFILDIOYAPEVSVTGDNFVGRKGVNLKCNADANPPFPKS | 302 |
| Db | 220 | SLACIVNHYM--DRFKESLTINVQYEPEVTIEGPDGNWYLQRMVMDVKLTCKADANPPATEY | 277 |
| Qy | 303 | VMSRLDQWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQKVIYISDVFPFKQ | 362 |
| Db | 278 | HWITLNGSLPKGVDAQNRTLFFPKGPINYSIAGTYICATNPIGTRSGQVEVNTFEFPTP | 337 |
| Qy | 363 | TS-----STIAGAVAGVAVLALFIIAIFVTVLLTPRKK--RPSYLDK----- | 402 |

```
Db 338 SPEHGRAGPVPTAIGGVAGSILLVIVGGIVVALRRRTFKGDYSTKHHVYNGY 397
Qy 403 -VIDLPPTHKPPLYEERSPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNLSRFDY 461
Db 398 SKAGIPQHH--PPMAQNLPDSDSD--EKKAGPLGGS-----SYEE 435
Qy 462 EDENPVGEDGIQOM-----YPLYN-----OMCYQDRSPGKHQNNPKRV 501
Db 436 EEEEEGGGGRKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRTLGYQY---DPEQL 492
Qy 502 -----YIDPREHYV 510
Db 493 DLAEENVMSQDGSFISKKEWYV 514
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RESULT 2

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US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morlyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Charles J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723.368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4
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```
Query Match 21.7%; Score 588; DB 4; Length 517;
Best Local Similarity 30.1%; Pred. No. 1.3e-46;
Matches 151; Conservative 85; Mismatches 176; Indels 90; Gaps 15;

Qy 71 GKNVSLKCLIE---VNETHITQISWEKIHGKSSQTVAVHHPQYGSVOGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKONVAIYNPSMGVSVLAPYRVERFLRPS 103

Qy 128 LNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVPEVTSILKGPDSLDG--- 184
Db 104 FTDGTIRLSRLEDEGVYCEPATFTGNRESQNLNTVMAKPT-NWIEGTQAVLRAKKG 162

Qy 185 -GNETVAACIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTFRFAGR 242
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQIEIRNPNGTIVTISRVLVPSREAHQ 222

Qy 243 RITCVVHPALEKDIRYSFILDIOYAPEVSVTVGDGNVFGVRKGVNLKCNADANPPPFKS 302
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQIEIRNPNGTIVTISRVLVPSREAHQ 222

Qy 243 RITCVVHPALEKDIRYSFILDIOYAPEVSVTVGDGNVFGVRKGVNLKCNADANPPPFKS 302
Db 223 SLACIVNYHM--DRFKESLTINVQYEPVETIEGDNWYIQRMDVKLTCKADANPPATEY 280

Qy 303 VWSRLDGOWPDGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQORSQDKYIYISDVFPKQ 362
Db 281 HWTTLNGLSPKGVQEAQNRITLFFKGPINYSLAGTYICEATNPIGTRSQVENVITEKPRPQ 340

Qy 363 TSIAVAGAVIGAVLALFIATFVTV--LLTPRKPSYLDKV-IDLPPTHKPPPLYEER 419
Db 281 HWTTLNGLSPKGVQEAQNRITLFFKGPINYSLAGTYICEATNPIGTRSQVENVITEKPRPQ 340

Qy 363 TS-----STAVAGAVIGAVLALFIATFVTVLLTPRKK--RPSYLDK----- 402
```

```
Db 341 SPEHGRAGPVPTAIGGVAGSILLVIVGGIVVALRRRTFKGDYSTKHHVYNGY 400
Qy 403 -VIDLPPTHKPPLYEERSPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNLSRFDY 461
Db 401 SKAGIPQHH--PPMAQNLPDSDSD--EKKAGPLGGS-----SYEE 438
Qy 462 EDENPVGEDGIQOM-----YPLYN-----OMCYQDRSPGKHQNNPKRV 501
Db 439 EEEEEGGGGRKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRTLGYQY---DPEQL 495
Qy 502 -----YIDPREHYV 510
Db 496 DLAEENVMSQDGSFISKKEWYV 517

RESULT 3
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6459155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular Localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1
```

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Query Match 21.8%; Score 584.5; DB 4; Length 458;
Best Local Similarity 35.5%; Pred. No. 2.4e-46;
Matches 137; Conservative 67; Mismatches 165; Indels 17; Gaps 9;

Qy 71 GKNVSLKCLIE---VNETHITQISWEKIHGKSSQTVAVHHPQYGSVOGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKONVAIYNPSMGVSVLAPYRVERFLRPS 103

Qy 128 LNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVPEVTSILKGPDSLDG--- 184
Db 104 FTDGTIRLSRLEDEGVYICGPFATFTGNRESQNLNTVMAKPT-NWIEGTQAVLRAKKG 162

Qy 185 -GNETVAACIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTFRFAGR 242
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQIEIRNPNGTIVTISRVLVPSREAHQ 222

Qy 243 RITCVVHPALEKDIRYSFILDIOYAPEVSVTVGDGNVFGVRKGVNLKCNADANPPPFKS 302
Db 223 SLACIVNYHM--DRFKESLTINVQYEPVETIEGDNWYIQRMDVKLTCKADANPPATEY 280

Qy 303 VWSRLDGOWPDGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQORSQDKYIYISDVFPKQ 362
Db 281 HWTTLNGLSPKGVQEAQNRITLFFKGPINYSLAGTYICEATNPIGTRSQVENVITEKPRPQ 340

Qy 363 TSIAVAGAVIGAVLALFIATFVTV--LLTPRKPSYLDKV-IDLPPTHKPPPLYEER 419
Db 341 RGLGSAARLLAGTVAVFLILVAVTLVFFLYNRQOKGPPETDAGTDQPLSQKPEPSPSRQ 400

Qy 420 SPPLPQKDLFQPBHL-PLQTFKERE 444
```



```
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match      16.9%; Score 458.5; DB 4; Length 479;
Best Local Similarity 30.2%; Pred. No. 2e-34;
Matches 121; Conservative 66; Mismatches 160; Indels 53; Gaps 13;

QY 33 PPTPPPLLLPFLPFLSRL-CGALAGPIIVEPHVTAVMGKNVSLKCLI---EWNETITQ 88
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 PPTP-----LLWPLLLLLLLETGAQDVRVQVLPVVRGQLGGTVLPCHLLPPVPGLYISL 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 89 ISWEKHGKSS-OTVAVHHPQYGFSGVQGYQG--RVLP-----KNYSINDATITL 135
   :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 68 VTQRPDAPANHONVAAPHKMGSPSPKPGSERLSFVSAKQSTQDTEAELQDATLAL 127
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 136 HNIQFSDSGKYICKAVTFPLGNAQSSTTVTVLVLP-----TVSLIKGPDLSLIDGNET 188
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 128 HGLTVEDEGNYTCEFAFPKGSVRGMTWLRIAKPKNQAEAKVTFSDP-----T 178
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 189 VAAICIAATGKPVAAHI-----DWEGLGEMESTTTTSFPNETATIIISQYKLFPTFRFARGR 242
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG---TWTVTSRFTLVPSGRADGV 234
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVGTGDNWFGVGRKGNLKNADANPPFPKS 302
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 235 TVTCKVEHSEFEPALIPVTLVSRYPPEVSIISGDDNWLGRDTATLSCDVRNSNPBTGY 294
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIYISDVFPFKQ 362
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 295 DWSTTSGTFTSAVAGSQL-VIHAVDSLENTTFCVTITNAVGMGRAEQVIFVRETPRAS 353
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 363 TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
   :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 354 PRDVGPLVWGAVGTTLLVLLLAGGSLAFILLRVRERRKS 393
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 7
US-09-949-016-6278
; Sequence 6278, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6278
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-6278

Query Match      15.1%; Score 409; DB 4; Length 456;
Best Local Similarity 28.3%; Pred. No. 8.7e-30;
Matches 119; Conservative 70; Mismatches 184; Indels 48; Gaps 14;

QY 4 TPGSPCLCPGG-----GKA-----QLSASLLGA-GLLLQPTPTPPLL 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 TPGTGAAPRGFQDLSSGWSWTRSDRGASRRRARRPREAQLIGATGMARAAAAPLL 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 41 LLLFPPLLSRLCGALAGPIIVE--PHVTAVMGKNVSLKCLIEVNET----ITQISWEKI 94
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 81 LVALLVLSWP---PPGTGDVVVQAPQVPGFLGDSVTLPCYLOVPMNEVTHVSQITWAR- 136
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 95 HGKSSQTVAVHH---PQYGFVQGYQGRVLFKNYSINDATITLHNIQFSDSGKYICKAV 151
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
```

```
US-09-949-016-6278

Query Match      16.9%; Score 458.5; DB 4; Length 479;
Best Local Similarity 30.2%; Pred. No. 2e-34;
Matches 121; Conservative 66; Mismatches 160; Indels 53; Gaps 13;

QY 33 PPTPPPLLLPFLPFLSRL-CGALAGPIIVEPHVTAVMGKNVSLKCLI---EWNETITQ 88
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 PPTP-----LLWPLLLLLLLETGAQDVRVQVLPVVRGQLGGTVLPCHLLPPVPGLYISL 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 89 ISWEKHGKSS-OTVAVHHPQYGFSGVQGYQG--RVLP-----KNYSINDATITL 135
   :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 68 VTQRPDAPANHONVAAPHKMGSPSPKPGSERLSFVSAKQSTQDTEAELQDATLAL 127
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 136 HNIQFSDSGKYICKAVTFPLGNAQSSTTVTVLVLP-----TVSLIKGPDLSLIDGNET 188
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 128 HGLTVEDEGNYTCEFAFPKGSVRGMTWLRIAKPKNQAEAKVTFSDP-----T 178
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 189 VAAICIAATGKPVAAHI-----DWEGLGEMESTTTTSFPNETATIIISQYKLFPTFRFARGR 242
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG---TWTVTSRFTLVPSGRADGV 234
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVGTGDNWFGVGRKGNLKNADANPPFPKS 302
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 235 TVTCKVEHSEFEPALIPVTLVSRYPPEVSIISGDDNWLGRDTATLSCDVRNSNPBTGY 294
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIYISDVFPFKQ 362
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 295 DWSTTSGTFTSAVAGSQL-VIHAVDSLENTTFCVTITNAVGMGRAEQVIFVRETPRAS 353
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 363 TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 398
   :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 354 PRDVGPLVWGAVGTTLLVLLLAGGSLAFILLRVRERRKS 393
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 8
US-09-949-016-7564
; Sequence 7564, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7564
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-7564

Query Match      15.1%; Score 409; DB 4; Length 456;
Best Local Similarity 28.3%; Pred. No. 8.7e-30;
Matches 119; Conservative 70; Mismatches 184; Indels 48; Gaps 14;

QY 4 TPGSPCLCPGG-----GKA-----QLSASLLGA-GLLLQPTPTPPLL 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 TPGTGAAPRGFQDLSSGWSWTRSDRGASRRRARRPREAQLIGATGMARAAAAPLL 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 41 LLLFPPLLSRLCGALAGPIIVE--PHVTAVMGKNVSLKCLIEVNET----ITQISWEKI 94
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 81 LVALLVLSWP---PPGTGDVVVQAPQVPGFLGDSVTLPCYLOVPMNEVTHVSQITWAR- 136
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 95 HGKSSQTVAVHH---PQYGFVQGYQGRVLFKNYSINDATITLHNIQFSDSGKYICKAV 151
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
```

Db 137 HGESGMAVPHQTQGPSYSESKRLEFVAARL--GAELRNASLRMFLGRVEDEGNYTCLFV 194
Qy 152 TFPPLGNAQSSTTVTVLVBP--TVSLIKGPDLSLDGNETVAAICIAATGKPVVAHIDWEGD 209
Db 195 TFPQGRSRVDIWLRLVAKPQNTAEVQKVOLT----GEPVPMARCVSTGGRPPAQITWHS 250
Qy 210 LGEMESTT--TSFPNETATISQYKLFPTFRFARGRRITCVVVKHPALEKDIRYSFILDIOY 267
Db 251 LGGMPTSOVPGFLSGTIVTSLWILVPSSQVDGKNTCKVEHESFEKPOLLTVNLTVY 310
Qy 268 APEVSVTGYDGNWFGVGRGVNLCNADANPPFKSVMSRLDQWPDGGLASDNTLHFVHP 327
Db 311 PPEVSIISGYNWYLGQNEATLTCDAENPBEPTGYNNSTTGMPLPPFAVAQAQL-LIRP 369
Qy 328 LTFNYSYGVICKVNTSLGQSDOKVIYISDVPPKQTSIAVAGAVIGAVLALFIAIFVT 387
Db 370 VDKINTTLCNVNMGARQALTVQVKEGPPSEHSGMS--RNAIIFVLGILVFLILLG 428
Qy 388 V 388
Db 429 I 429

RESULT 9
US-09-949-016-6729
; Sequence 6729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6729
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6729

Query Match 14.8%; Score 402; DB 4; Length 417;
Best Local Similarity 29.3%; Pred. No. 3.5e-29;
Matches 106; Conservative 67; Mismatches 163; Indels 26; Gaps 11;

Qy 44 PPLLLFSRLCGAL----AGPIIVE--PHVTAVWGKNSLKLIEVNET---ITQISWEK 93
Db 9 WPLLLVALLVSWPPPGTGDVVVQAPTQVPLGDSVTLPCVLQVPMNEVTHVSQLTWTR 68
Qy 94 IHGKSSQTVAVHH---POYGFVSQGEYQGRVLFKNYSLNDATITLHNIQFSDSGKYICKA 150
Db 69 -HGESGMAVPHQTQGPSYSESKRLEFVAARL--GAELRNASLRMFLGRVEDEGNYTCLF 125
Qy 151 VTFPLGNAQSSTTVTVLVBP--TVSLIKGPDLSLDGNETVAAICIAATGKPVVAHIDWEG 208
Db 126 VTFPQGRSRVDIWLRLVAKPQNTAEVQKVOLT----GEPVPMARCVSTGGRPPAQITWHS 181
Qy 209 DLGEMESTT--TSFPNETATISQYKLFPTFRFARGRRITCVVVKHPALEKDIRYSFILDIO 266
Db 182 DLGGMPTSOVPGFLSGTIVTSLWILVPSSQVDGKNTCKVEHESFEKPOLLTVNLTVY 241
Qy 267 YAPEVSVTGYDGNWFGVGRGVNLCNADANPPFKSVMSRLDQWPDGGLASDNTLHFVHP 326
Db 242 YPPEVSIISGYNWYLGQNEATLTCDAENPBEPTGYNNSTTGMPLPPFAVAQAQL-LIR 300

Qy 327 PLTFNYSYGVICKVNTSLGQSDOKVIYISDVPPKQTSIAVAGAVIGAVLALFIAIFV 386
Db 301 PVDKINTTLCNVNMGARQALTVQVKEGPPSEHSGMS--RNAIIFVLGILVFLILL 359
Qy 387 TV 388
Db 360 GI 361

RESULT 10
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match 14.8%; Score 400.5; DB 3; Length 408;
Best Local Similarity 30.8%; Pred. No. 4.6e-29;
Matches 123; Conservative 64; Mismatches 167; Indels 45; Gaps 14;

Qy 17 AQLSSASLLGAGLLLPPTPPPLLLPLLLFRLRCAL--AG---PIIVPEHVTAVWG 71
Db 2 AQLARAT-----RSPLSWLLLF-----CYALRKAGGDIRVLVPYNSTGVLG 43
Qy 72 KNVSLKCLIEVNE--TITQISW-EKHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSL 128
Db 44 GSTTLHCSLTSENENVTITQITMMKDSGGSHALVAFHPKGPNIKEPERVKFLAAQODL 103
Qy 129 NDATITLHNIQFSDGKYICKAVTFPLGNAQSSTTVTVLVBP--TVSLIKGPDLSLI--DG 184
Db 104 RNASIAISNLSVEDEGIYEQIATFPGRSSTNWLKVQARPKNATAEALESPTLLIQD- 162
Qy 185 GNETVAAICIAATGKPVVAHIDW----EGDLGEMESTTTSFPNETATISQYKLFPTFRPAR 240
Db 163 -----VAKCISANGHPGGRISWPSNVNGSHREKKE-FCGQPG-TTIVTSYLSMVPQRQAD 215
Qy 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFGVGRGVNLCNADANPPP 299
Db 216 GKNITCTVEHESLQELDQLLVTLTSQPYPPENSVISGYDGNWYVGLTNLTLTCEAHSKAP 275
Qy 300 FKS--VMSRLDQWPDGGLASDNTLHFVHPITFNYSGYICKVNTSLGQSDOKVIYISD 357
Db 276 DMAGYNNSTNTGDPFNSVYKRGQNNMLISTVEDGLNNTVIVCEVTNALGSGQGVHIIVKE 335
Qy 358 VPFQKQTSIAVAGAVIGAVLALFIAIFVTVLTPRKKR 396
Db 336 KPENNQONTRLHLGLYIFLIVFLAVVILIAALYIIRCCR 374

RESULT 11
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510

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; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

Query Match 11.3%; Score 306.5; DB 4; Length 442;
Best Local Similarity 25.0%; Pred. No. 3.9e-20;
Matches 106; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

QY 8 SPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLLPPLLSRLCGALAGPIIVEPHVT 67
DB 3 SVVLPSGSQCAAAAAAAPPGLRLR-----LLLLLFS-----AALPTGQGNLFTKQDVT 53
QY 68 AVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGEYQGRVLFKNYS 127
DB 54 VIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLNFS 103
QY 128 LNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDGNN 186
DB 104 SSELKVLSTNVISDEGRYFCQLYTD--POESYTTITVLVPPRNLMDIQKTAVEG-- 159
QY 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMSTTTTSPNETATIIISQYKLFPTFRAR 240
DB 160 EIEVNCNTMASKPATIRFKGNTELKKGSEVEEWSDMY-----TVTSQMLKXVHKEDD 214
QY 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNMFVGRKG--VNLKCNADANPP 298
DB 215 GVPVICOVEHPAVTGNLQYRLEVQYKQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
QY 299 PFKSVWSRLDQGWPDGLASDNTLHFVHPLTFNYSYGVYCKVNSLQGRSDQKVIYISDV 358
DB 275 PVMVTWVRVDDMPQHAFLSGPNL-FINNLTNDNGTYRCEASNIVGKAHSDYMLXYVDP 333
QY 359 PF-----KOTSSIAVAGAVIGAVLALFIIFVTVL 389
DB 334 PTTIPPTTTTTTTTTTTTTTTTTTTTITLTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLI 393
QY 390 LTPR 393
DB 394 ILGR 397

RESULT 12
US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 11.3%; Score 306.5; DB 4; Length 442;
Best Local Similarity 25.0%; Pred. No. 3.9e-20;
Matches 106; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

QY 8 SPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLLPPLLSRLCGALAGPIIVEPHVT 67
DB 3 SVVLPSGSQCAAAAAAAPPGLRLR-----LLLLLFS-----AALPTGQGNLFTKQDVT 53
QY 68 AVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGEYQGRVLFKNYS 127
DB 54 VIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLNFS 103
QY 128 LNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDGNN 186
DB 104 SSELKVLSTNVISDEGRYFCQLYTD--POESYTTITVLVPPRNLMDIQKTAVEG-- 159
QY 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMSTTTTSPNETATIIISQYKLFPTFRAR 240
DB 160 EIEVNCNTMASKPATIRFKGNTELKKGSEVEEWSDMY-----TVTSQMLKXVHKEDD 214
QY 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNMFVGRKG--VNLKCNADANPP 298
DB 215 GVPVICOVEHPAVTGNLQYRLEVQYKQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
QY 299 PFKSVWSRLDQGWPDGLASDNTLHFVHPLTFNYSYGVYCKVNSLQGRSDQKVIYISDV 358
DB 275 PVMVTWVRVDDMPQHAFLSGPNL-FINNLTNDNGTYRCEASNIVGKAHSDYMLXYVDP 333
QY 359 PF-----KOTSSIAVAGAVIGAVLALFIIFVTVL 389
DB 334 PTTIPPTTTTTTTTTTTTTTTTTTTTITLTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLI 393
QY 390 LTPR 393
DB 394 ILGR 397

RESULT 13
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 11.2%; Score 304.5; DB 4; Length 440;
Best Local Similarity 25.2%; Pred. No. 6e-20;
Matches 108; Conservative 76; Mismatches 167; Indels 77; Gaps 16;

QY 8 SPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLLPPLLSRLCGALAGPIIVEPHVT 67

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Db 3 SVVLPSSGQCAAAA-----AAPPGLRL-----LLFS--AAALITGQGNLFT 47
Qy 64 PHVAVMGKNSVSKLIEVNETITQISWEKIHGKSQTVAVHHPPQYGFSGQGRVLF 123
Db 48 KDVTVIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YPRDFRPLKDSRQL 97
Qy 124 KNSLNDATITLHNGFSDSGKYCKAVTFPLGNAQSSTTVVLVEPVSILIK-GPDSL 182
Db 98 LNFSSSELKSLTNVSDSGRYFCQLYDTP--PQESYTTITVLVPPNLMIDIKDTAV 155
Qy 183 DGNGETVAACIAATGKPAHIDW-EGDL-----GEMESTTTSFPNETATISQVKLPPT 236
Db 156 EG--EEIEVNTAMASKPATIRFKNGTELKGSVEWDMY-----TWSQLMLKVH 208
Qy 237 RFARRRITCVVHKPALEKDIRYGFILDIQVAPEVSVTGYDGNWFGVGRKG--VNLKCNAD 294
Db 209 KEDDGPVVCQVEHPAVTGNLTQRYLEVQKPVQHIQMTYPLQGLTREGDALELTCEAI 268
Qy 295 ANPPFKSVNRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIY 354
Db 269 GKPOQVMTVVRVDEMPQHAVLSPNL-FINNLNKTNDGTGRCEASIVGKAHSDYMLY 327
Qy 355 ISDVPF-----KOTSSIAVAGAVIGAVLALFIIAIF 385
Db 328 VYDPTPIPTTTTTTTTTTTTTTTTTTTITSDRAGEGSIKRAVDHAVIGGVAVVFWFAML 387
Qy 386 VTLLTPR 393
Db 388 CLLIILGR 395

RESULT 14

US-09-944-457-61
; Sequence 61, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 15, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-61

Query Match 11.2%; Score 304.5; DB 4; Length 440;
Best Local Similarity 25.2%; Pred. No. 6e-20;
Matches 108; Conservative 76; Mismatches 167; Indels 77; Gaps 16;
Qy 8 SPLCPGGKQALSSALGAGLLLPPTPPPLLLPFLLLFSRLCGALA----GPIIVE 63

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Db 3 SVVLPGSQCAAAA-----AAPPGLRL---LLFS--AAALPTGGQNLFT 47
Qy 64 PHVTAVMGKNSVKCLIEVNETITQISWEKHGKSQTVAVHHPOYGFVSQGEYQGRVLF 123
Db 48 KDVTVIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDPRPLKDSRFQL 97
Qy 124 KNSLNDATITLHNIGFSDGKVIKCAVTPPLGNAQSSITVTLVVEPTVSLIK-GPDSL 182
Db 98 LNFSSSELKVSILNVSISDEGRYFCOLYTDp--POESYTTITVLVPPRNLMDIQD 155
Qy 183 DGCNETVAAICIAATGKPAHIDW-EGDL-----GEMESTTTSFPNETATII 236
Db 156 EG--EEIEVNCAMASKPATIIRFKGTELKSEVEWSDMY-----TVTSQMLMKVH 208
Qy 237 RFARGRRITCVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVRKG--VNLKCNAD 294
Db 209 KEDGVPVICQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPLQGLTREGDALELTCEAI 268
Qy 295 ANPPPKSVWSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVY 354
Db 269 GKQPVMVTWVRVDDENPQHAVLSGPNL-FINNLTNDNGTYRCEASNIVGKAHSDYMLY 327
Qy 355 ISDVPF-----KOTSSIAVAGAVIGAVLALFIIAIF 385
Db 328 VYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 387
Qy 386 VTLLTPR 393
Db 388 CLLIILGR 395

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RESULT 15

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US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-778-510-22

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Query Match 10.7%; Score 290.5; DB 4; Length 423;
Best Local Similarity 25.7%; Pred. No. 1.2e-18;
Matches 102; Conservative 71; Mismatches 165; Indels 59; Gaps 14;

Qy 36 PPPL-LLLLPPLLFSLRCLGALAGPIIVEPHTAVWGKNSVKCLIEVNETITQISWEKI 94
Db 3 PPGLRLRLLLLLSAAALIPFGDQONLFTKDVTVIEGEVATISC--QVNKSDSVI--QL 58
Qy 95 HGKSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATITLHNIGFSDGKVIKCAVTFP 154
Db 59 LNPNRQTI-----YFRDPRPLKDSRFQLLNFSSELKVSILNVSISDEGRYFCOLYTD 112
Qy 155 LGNAQSSITVTLVVEPTVSLIK-GPDSLIDGNETVAAICIAATGKPAHIDW-EGD--- 209
Db 113 --POESYTTITVLVPPRNLMDIQD TAVEG--BEIEVNCAMASKPATIIRWFKGNKEL 168
Qy 210 --LGEMESTTTSFPNETATIIISQVKLPFTRFARGRRITCVKHPALEKDIRYSFILD 267
Db 169 KGKSEVEWSDMY-----TVTSQMLMKVHKEDDGVVPVICQVEHPAVTGNLQOTRYLEV 223

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Qy 268 APEVSVTGYDGNWFGVRKG--VNLKCNADANPPPKSVWSRLDQGWPDGLASDNTLHFV 325
Db 224 KQVHIQMTYPLQGLTREGDAFELTCEALGKQOPVMVTWVRVDDENPQHAVLSGPNL-FI 282
Qy 326 HPLTFNYSGVYICKVTNSLQGRSDQKVYISDVP-----FKQTSI----- 366
Db 283 NNLNKTNDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTILTI 342
Qy 367 -----AVAGAVIGAVLALFIIAIFVTVLLTPR 393
Db 343 SRAGEBTTCIAVDHAVIGGVAVVWFAMLCIIILGR 379

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Search completed: October 6, 2005, 09:44:22
Job time : 22.3581 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 237.135 Seconds
(without alignments)
894.712 Million cell updates/sec

Title: US-09-972-268-10
Perfect score: 2711
Sequence: 1 MARTPGSPICPGGKQAQLS.....KHQNDPKRVYIDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 2711 | 100.0 | 510 | 10 | US-09-972-268-10 |
| 2 | 2693 | 99.3 | 510 | 10 | US-09-972-268-12 |
| 3 | 2679 | 98.8 | 504 | 10 | US-09-972-268-8 |
| 4 | 2406 | 88.7 | 510 | 10 | US-09-959-845-4 |
| 5 | 2406 | 88.7 | 510 | 10 | US-09-972-268-18 |
| 6 | 2243 | 82.7 | 437 | 10 | US-09-972-268-31 |
| 7 | 2125 | 78.4 | 438 | 10 | US-09-959-845-6 |
| 8 | 2125 | 78.4 | 438 | 10 | US-09-972-268-19 |
| 9 | 1932 | 71.3 | 595 | 10 | US-09-972-268-14 |
| 10 | 1930 | 71.2 | 387 | 10 | US-09-972-268-16 |
| 11 | 1924.5 | 71.0 | 549 | 10 | US-09-972-268-4 |
| | | | | | Sequence 10, Appl |
| | | | | | Sequence 12, Appl |
| | | | | | Sequence 8, Appl |
| | | | | | Sequence 4, Appl |
| | | | | | Sequence 18, Appl |
| | | | | | Sequence 31, Appl |
| | | | | | Sequence 6, Appl |
| | | | | | Sequence 19, Appl |
| | | | | | Sequence 14, Appl |
| | | | | | Sequence 16, Appl |
| | | | | | Sequence 4, Appl |

12 1906.5 70.3 549 10 US-09-972-268-6
13 1906.5 70.3 549 14 US-10-161-572-45
14 1903.5 70.2 634 10 US-09-972-268-13
15 1898 70.0 426 10 US-09-972-268-15
16 1885.5 69.5 542 10 US-09-972-268-2
17 1837.5 67.8 549 10 US-09-959-845-2
18 1837.5 67.8 549 10 US-09-972-268-17
19 588 21.7 514 14 US-10-161-572-60
20 588 21.7 517 10 US-09-972-268-20
21 587.5 21.7 458 10 US-09-972-268-21
22 565.5 20.9 518 9 US-09-919-172-20
23 565.5 20.9 518 16 US-10-752-986-20
24 540 19.9 530 18 US-10-631-467-1474
25 538.5 19.9 485 15 US-10-422-571-15
26 538.5 19.9 485 15 US-10-422-571-33
27 538.5 19.9 485 15 US-10-422-571-114
28 538.5 19.9 485 15 US-10-422-571-116
29 538.5 19.9 485 15 US-10-422-571-129
30 538.5 19.9 497 10 US-09-972-268-37
31 537 19.8 498 10 US-09-972-268-39
32 527.5 19.5 510 15 US-10-422-571-5
33 527.5 19.5 510 15 US-10-422-571-31
34 527 19.4 538 10 US-09-972-268-23
35 527 19.4 538 10 US-09-984-130-138
36 527 19.4 538 10 US-09-836-353A-138
37 527 19.4 538 14 US-10-161-572-61
38 527 19.4 538 15 US-10-411-010-17
39 527 19.4 538 17 US-10-953-264-17
40 524 19.3 510 15 US-10-422-571-25
41 524 19.3 510 15 US-10-422-571-36
42 523.5 19.3 510 10 US-09-766-511B-33
43 523.5 19.3 510 14 US-10-241-220-94
44 523.5 19.3 510 15 US-10-295-027-66
45 523.5 19.3 510 15 US-10-173-999-76

ALIGNMENTS

RESULT 1

US-09-972-268-10
; Sequence 10 Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE 1
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are from human Nectin-3 beta
US-09-972-268-10

Query Match 100.0%; Score 2711; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 8e-198;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARTPGSPICPGGKQAQLSSASLLGALLQPTPPPLLLLLLFFLLFSLCGALAGPI 60
Db 1 MARTPGSPICPGGKQAQLSSASLLGALLQPTPPPLLLLLLFFLLFSLCGALAGPI 60

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QY 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
DB 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPD 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
DB 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
QY 241 GRRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
DB 241 GRRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPF 360
DB 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPF 360
QY 361 KOTSSIAVAGAVIGAVLAFIIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
DB 361 KOTSSIAVAGAVIGAVLAFIIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
QY 421 PPLPQKDLFQPEHLPLQTOFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIOQMYPLYN 480
DB 421 PPLPQKDLFQPEHLPLQTOFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIOQMYPLYN 480
QY 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510
DB 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510

RESULT 2
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972.268
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match 99.3%; Score 2693; DB 10; Length 510;
Best Local Similarity 99.6%; Pred. No. 1.9e-196;
Matches 508; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARTPSPSPCPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLFRLCAGLAGPI 60
DB 1 MARTLSPSPCPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLFRLCAGLAGPI 60
QY 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
DB 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPD 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPD 180

QY 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
DB 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPD 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPD 180
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QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
DB 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
QY 241 GRRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
DB 241 GRRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPF 360
DB 301 KSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPF 360
QY 361 KOTSSIAVAGAVIGAVLAFIIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
DB 361 KOTSSIAVAGAVIGAVLAFIIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
QY 421 PPLPQKDLFQPEHLPLQTOFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIOQMYPLYN 480
DB 421 PPLPQKDLFQPEHLPLQTOFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIOQMYPLYN 480
QY 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510
DB 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510

RESULT 3
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972.268
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match 98.8%; Score 2679; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.2e-195;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PSLPCPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLFRLCAGLAGPIIIVPHV 66
DB 1 PSLPCPGGKQAQLSSASLLGAGLLLOPPTPPPLLLLFRLCAGLAGPIIIVPHV 60
QY 67 TAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGRVLFKNY 126
DB 61 TAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQYQGRVLFKNY 120
QY 127 SLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPDSLIDGN 186
DB 121 SLNDATITLHNIGFSDSGKYICKAVTFFLGNAQSSQTVVHVEPTVSLIKGPDSLIDGN 180
QY 187 ETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRITC 246
DB 181 ETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRITC 240
QY 247 VVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVWSR 306
DB 241 VVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVWSR 300
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Qy 307 LDGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDQKVIYISDVPPKQTSSI 366
 Db 301 LDGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDQKVIYISDVPPKQTSSI 360
 Qy 367 AVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQK 426
 Db 361 AVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQK 420
 Qy 427 DLFOPEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPLYNQMCYQD 486
 Db 421 DLFOPEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPLYNQMCYQD 480
 Qy 487 RSPGKHQNDPKRVIYIDPREHYV 510
 Db 481 RSPGKHQNDPKRVIYIDPREHYV 504

RESULT 4
 US-09-959-845-4
 ; Sequence 4, Application US/09959845
 ; Publication No. US20030008334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yoehimi TAKAI
 ; APPLICANT: Hiroyuki NAKANISHI
 ; APPLICANT: Keiko SATO
 ; APPLICANT: Kenichi TAKAHASHI
 ; TITLE OF INVENTION: Protein Nectin-3
 ; FILE REFERENCE: 2001-1678A/LC/00653
 ; CURRENT APPLICATION NUMBER: US/09/959,845
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: PCT/JP01/01871
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: JP 2000-065595
 ; PRIOR FILING DATE: 2000-03-09
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patentin ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 510
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-09-959-845-4

Query Match 88.7%; Score 2406; DB 10; Length 510;
 Best Local Similarity 89.2%; Pred. No. 1.4e-174;
 Matches 456; Conservative 22; Mismatches 31; Indels 2; Gaps 2;
 Qy 1 MARTPGSPICPGGKAQLSSASLLGALLLOPTPPPLLLLLLFPILLFSLRCGALAGPI 60
 Db 1 MARTPGPAPLCPGGKAQLSSAFPPAAGLLLPAPTPPPLLLLLLFPILLFSLRCGALAGSI 60
 Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSVOGEYQGR 120
 Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGSVOGDYQGR 120
 Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDS 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDS 180
 Qy 181 LIDGGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
 Db 181 LIDGGNETVAACVAATGKPAQIDWEGDLGEMESTTSPNETATIVSQYKLPPTFRAR 240
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTYGDNWFGVGRKGNLKNADANPPPF 300
 Db 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTYGDNWFGVGRKGNLKNADANPPPF 300
 Qy 301 KSVMSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDQKVIYISDVPP 360
 Db 301 KSVMSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDQKVIYISDIPL 360
 Qy 361 KOTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
 Db 361 KOTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
 Qy 421 PPLPQKDLF-QPEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPL 479
 Db 421 PSLPQKDLGLQTEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPL 480
 Qy 480 NQMCYQDRSPGKHQNDPKRVIYIDPREHYV 510

Db 361 QTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
 Qy 421 PPLPQKDLF-QPEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPL 479
 Db 421 PSLPQKDLGLQTEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPL 480
 Qy 480 NQMCYQDRSPGKHQNDPKRVIYIDPREHYV 510
 Db 481 SQMCHQDRSPRQHHPRN-PERLYINPREHYV 510

RESULT 5
 US-09-972-268-18
 ; Sequence 18, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanelow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TI
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,557
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 510
 ; TYPE: PRT
 ; ORGANISM: mus musculus
 US-09-972-268-18

Query Match 88.7%; Score 2406; DB 10; Length 510;
 Best Local Similarity 89.2%; Pred. No. 1.4e-174;
 Matches 456; Conservative 22; Mismatches 31; Indels 2; Gaps 2;
 Qy 1 MARTPGSPICPGGKAQLSSASLLGALLLOPTPPPLLLLLLFPILLFSLRCGALAGPI 60
 Db 1 MARTPGPAPLCPGGKAQLSSAFPPAAGLLLPAPTPPPLLLLLLFPILLFSLRCGALAGSI 60
 Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSVOGEYQGR 120
 Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGSVOGDYQGR 120
 Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDS 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGSDS 180
 Qy 181 LIDGGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
 Db 181 LIDGGNETVAACVAATGKPAQIDWEGDLGEMESTTSPNETATIVSQYKLPPTFRAR 240
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTYGDNWFGVGRKGNLKNADANPPPF 300
 Db 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTYGDNWFGVGRKGNLKNADANPPPF 300
 Qy 301 KSVMSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDQKVIYISDVPP 360
 Db 301 KSVMSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDQKVIYISDIPL 360
 Qy 361 KOTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
 Db 361 KOTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
 Qy 421 PPLPQKDLF-QPEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPL 479
 Db 421 PSLPQKDLGLQTEHLPLQTOFKEREVGNLQHSNGLNRSFDYEDENPVGEDGIQOMYPL 480
 Qy 480 NQMCYQDRSPGKHQNDPKRVIYIDPREHYV 510

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Db 481 SQMCHQDRSPRQHPRN-PERLYNPREHYV 510

RESULT 6
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match 82.7%; Score 2243; DB 10; Length 437;
Best Local Similarity 99.5%; Pred. No. 2.9e-162;
Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTPGSPICPGGKAQLSSASLLGAGLLLOPPTPPPLLLLLLFPPLLSRLCGALAGPI 60
Db 1 MARTLPSPLCPGGKAQLSSASLLGAGLLLOPPTPPPLLLLLLFPPLLSRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
Qy 361 KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPVSLDKVIDLPPTHKPPPLYEERS 420
Db 361 KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPVSLDKVIDLPPTHKPPPLYEERS 420
Qy 421 PPLPQKDLFQ 430
Db 421 PPLPQKDLFQ 430

RESULT 7
US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hirovuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
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; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

Query Match 78.4%; Score 2125; DB 10; Length 438;
Best Local Similarity 93.7%; Pred. No. 2.9e-153;
Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MARTPGSPICPGGKAQLSSASLLGAGLLLOPPTPPPLLLLLLFPPLLSRLCGALAGPI 60
Db 1 MARTPGAPLCPGGKAQLSSAPPAAGLLLPAPTTPPLLLLLLFPPLLSRLCGALAGSI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFSGVQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDIPL 360
Qy 361 KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPVSLDKVIDLPPTHKPPPLYEERS 420
Db 361 KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPVSLDKVIDLPPTHKPPPLYEERI 420
Qy 421 PPLPQKDL 428
Db 421 PSLPQKDL 428

RESULT 8
US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 438
```

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; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

Query Match      78.4%; Score 2125; DB 10; Length 438;
Best Local Similarity 93.7%; Pred. No. 2.9e-153;
Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MARTPGSPICPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPFLLLFRLCGALAGPI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARTPGSPICPGGKAQLSSAPPAAGLLLPAPTTPPLLLLPFLLLFRLCGALAGSI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDOKVIYISDVPF 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDOKVIYISDVPF 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 361 KOTSSIAVAGAVIGALVLAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 KOTSSIAVAGAVIGALVLAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERI 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 421 PPLPQKDL 428
    |||||:
Db 421 PSLPQKDL 428
    |||||:

RESULT 9
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match      71.3%; Score 1932; DB 10; Length 595;
Best Local Similarity 86.8%; Pred. No. 2.2e-138;
Matches 375; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

Qy 1 MARTPGSPICPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPFLLLFRLCGALAGPI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 1 MARTPGSPICPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPFLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYGR 120
Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Qy 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDOKVIYISDVPF 360
Db 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDOKVIYISDVPF 360
Qy 361 KOTSSIAVAGAVIGALVLAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KOTSSRS-----CDK-----THTCPCPAPEA 382
Qy 421 PPLPQKDLFOPE 432
Db 383 EGAPSVFLPPPK 394

RESULT 10
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match      71.2%; Score 1930; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.8e-138;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARTPGSPICPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPFLLLFRLCGALAGPI 60
Db 1 MARTPGSPICPGGKAQLSSASLLGAGLLQLQPTPPPLLLLPFLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYGR 120
Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

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QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRAR 240
 Db |||||
 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRAR 240
 QY 241 GRRITCVVHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
 Db |||||
 241 GRRITCVVHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
 QY 301 KSWMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP 360
 Db |||||
 301 KSWMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP 360
 QY 361 KQTSS 365
 Db |||||
 361 KQTSS 365
 RESULT 11
 US-09-972-268-4
 ; Sequence 4, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanslow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,557
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 549
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fro
 ; OTHER INFORMATION: m human Nectin-3 alpha
 US-09-972-268-4
 Query Match 71.0%; Score 1924.5; DB 10; Length 549;
 Best Local Similarity 67.9%; Pred. No. 7.3e-138;
 Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
 QY 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPILLFSLRCLGALAGPI 60
 Db |||||
 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPILLFSLRCLGALAGPI 60
 QY 61 IVEPHVTVAVGKGVNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
 Db |||||
 61 IVEPHVTVAVGKGVNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
 QY 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db |||||
 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRAR 240
 Db |||||
 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRAR 240
 QY 241 GRRITCVVHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
 Db |||||
 241 GRRITCVVHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
 QY 301 KSWMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP - 359
 Db |||||
 301 KSWMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPT 360
 QY 360 -----FKQTSIAVAGAVIGAVLALFIIA 383
 Db |||||
 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
 QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPPTHK-----PPPLYEERSPPLP 424

Db 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
 QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPPTHK-----PPPLYEERSPPLP 424
 Db 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQDELSDSYPSVKENKPNV- 478
 QY 425 QKDLQPEHL--PLOTQPKEREVGNLQHSNGLNSRSDYEDENPNVGEDIGQQMYPLYNQM 482
 Db 479 -NNLRKDYLEPEKTQW-----NNVENLRNF-ERPMDIYEDLKGMKMFVSD----- 523
 QY 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
 Db 524 -----EHYDENEDDLVSHVDGSGVISRREWV 549
 RESULT 12
 US-09-972-268-6
 ; Sequence 6, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanslow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,557
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 549
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-972-268-6
 Query Match 70.3%; Score 1906.5; DB 10; Length 549;
 Best Local Similarity 67.6%; Pred. No. 1.7e-136;
 Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;
 QY 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPILLFSLRCLGALAGPI 60
 Db |||||
 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPILLFSLRCLGALAGPI 60
 QY 61 IVEPHVTVAVGKGVNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
 Db |||||
 61 IVEPHVTVAVGKGVNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
 QY 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db |||||
 121 VLFKNYSLNDATITLHNI GFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRAR 240
 Db |||||
 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRAR 240
 QY 241 GRRITCVVHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
 Db |||||
 241 GRRITCVVHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
 QY 301 KSWMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP - 359
 Db |||||
 301 KSWMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPT 360
 QY 360 -----FKQTSIAVAGAVIGAVLALFIIA 383
 Db |||||
 361 TTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
 QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPPTHK-----PPPLYEERSPPLP 424

Db 421 VLAGIFCYRRRTFRGDFAKNY-IPPSDMQKESQIDVLQODELDSVPSVKKENKMPV- 478
Qy 425 QKOLFQPEHL--PLQTFKEREVGNLQHSNGLNRSFDEYDENPVGSDGIQQMYPLYNQM 482
Db 479 -NNLIRKDYLEPEKQW-----NNVENLNR-ERPMDYVEDLKMGKMFVSD----- 523
Qy 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
Db 524 -----EHYDENEDDLVSHVDGVSISRREWYV 549

RESULT 13

US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161.572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 70.3%; Score 1906.5; DB 14; Length 549;
Best Local Similarity 67.6%; Pred. No. 1.7e-136;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;
Qy 1 MARTPGSPCLPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLLSRLCAGAPI 60
Db 1 MARTLRSPCLPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLLSRLCAGAPI 60
Qy 61 IVEPHVTAVGKNVSKLCLEVNNTITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Db 61 IVEPHVTAVGKNVSKLCLEVNNTITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTFRAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNWFGVGRGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNWFGVGRGNLKNADANPPPF 300
Qy 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP- 359
Db 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPP 360
Qy 360 -----FKOTSSIAVAGAVICAVLALFIIA 383
Db 361 TTTTQIOWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVGGALFVLVS 420
Qy 384 IFVTVLLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPPLP 424

Db 421 VLAGIFCYRRRTFRGDFAKNY-IPPSDMQKESQIDVLQODELDSVPSVKKENKMPV- 478
Qy 425 QKOLFQPEHL--PLQTFKEREVGNLQHSNGLNRSFDEYDENPVGSDGIQQMYPLYNQM 482
Db 479 -NNLIRKDYLEPEKQW-----NNVENLNR-ERPMDYVEDLKMGKMFVSD----- 523
Qy 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
Db 524 -----EHYDENEDDLVSHVDGVSISRREWYV 549

RESULT 14

US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 70.2%; Score 1903.5; DB 10; Length 634;
Best Local Similarity 84.4%; Pred. No. 3.5e-136;
Matches 373; Conservative 7; Mismatches 43; Indels 19; Gaps 2;
Qy 1 MARTPGSPCLPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLLSRLCAGAPI 60
Db 1 MARTPGSPCLPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLLSRLCAGAPI 60
Qy 61 IVEPHVTAVGKNVSKLCLEVNNTITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Db 61 IVEPHVTAVGKNVSKLCLEVNNTITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTFRAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNWFGVGRGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNWFGVGRGNLKNADANPPPF 300
Qy 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
Db 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPT 360
Qy 361 KOTSSIAVAGAVICAVLALFIIIFVTVLLTPRKRSYLDKVIDL-----PPTH 410
Db 361 TTT-----LQPTIOWHPSTADIEDLATEPKLPPLSTLATIKDDTIATRSCKTH 411
Qy 411 KPPLYEERSPPLPKQDLFOPE 432
Db 412 TCPCCPAPEAGAPSVFLFPFK 433

RESULT 15
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match 70.0%; Score 1898; DB 10; Length 426;
Best Local Similarity 76.2%; Pred. No. 5.4e-136;
Matches 380; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

Qy 1 MARTPGSPICPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPPLLSRLCGALAGPI 60
Db 1 MARTPGSPICPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPPLLSRLCGALAGPI 60

Qy 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGSSQTVAVHHPOYGFVSQGEYQGR 120
Db 61 IVEPHVTAVMGKNSLKLIEVNETITQISWEKIHGSSQTVAVHHPOYGFVSQGEYQGR 120

Qy 121 VLFKNYSINDATITLHNIGFSDSKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTRFAR 240

Qy 241 GRRITCVVKKHPALEKDIRY3FILDIOYAPEVSVTYGDNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVKKHPALEKDIRY3FILDIOYAPEVSVTYGDNWFGVGRKGNLKNADANPPPF 300

Qy 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTNYSGVICKVTNSLQSRSDOKVIYISDVPF 360
Db 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTNYSGVICKVTNSLQSRSDOKVIYISDVPF 360

Qy 361 KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPR-KKRPVLDKVIDLPPTHKPPPLYEER 419
Db 360 -----TTTTLQPTIQWHPSTAD-IEDLATEPKKLP----- 388

Qy 420 SPPLPQKDLFQPEHLPIQT--QFYEREVGNLQHSNRSFYEDENPVGEDGIQOMYP 477
Db 389 -----FPLSTLATIKDDTIAT-----RSGSSDYKDD----- 415

Qy 478 LYNQMCYQDRSPGKHONN 496
Db 416 -----DKGSSHHHHH 426

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 84.2348 Seconds
(without alignments)
2341.642 Million cell updates/sec

Title: US-09-972-268-12
Perfect score: 2707

Sequence: 1 MARTLRSPICPGGKAQLS.....KHQNDPKVYIDPREHYV 510

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 2707 | 100.0 | 510 | 5 | Aae23286 Human nec |
| 2 | 2693 | 99.5 | 510 | 5 | Aae23285 Mouse nec |
| 3 | 2679 | 99.0 | 504 | 5 | Aae23284 Human del |
| 4 | 2388 | 88.2 | 510 | 4 | Aag63983 Amino aci |
| 5 | 2388 | 88.2 | 510 | 5 | Aae23292 Mouse nec |
| 6 | 2257 | 83.4 | 437 | 5 | Aae23299 Human nec |
| 7 | 2107 | 77.8 | 438 | 4 | Aag63984 Amino aci |
| 8 | 2107 | 77.8 | 438 | 5 | Aae23293 Mouse nec |
| 9 | 1920.5 | 70.9 | 549 | 5 | Aae23283 Human nec |
| 10 | 1920.5 | 70.9 | 549 | 6 | Abj20222 Human IG |
| 11 | 1920.5 | 70.9 | 549 | 8 | Adr66369 Human pro |
| 12 | 1920.5 | 70.9 | 549 | 8 | Adr66711 Human pro |
| 13 | 1914 | 70.7 | 595 | 5 | Aae23288 Human nec |
| 14 | 1912 | 70.6 | 387 | 5 | Aae23290 Human nec |
| 15 | 1906.5 | 70.4 | 549 | 5 | Aae23282 Mouse nec |
| 16 | 1895.5 | 69.7 | 542 | 5 | Aae23281 Human del |
| 17 | 1895.5 | 69.7 | 634 | 5 | Aae23287 Human nec |
| 18 | 1893.5 | 69.6 | 555 | 4 | Aam39143 Human pol |
| 19 | 1880 | 69.4 | 426 | 5 | Aae23289 Human nec |
| 20 | 1819.5 | 67.2 | 549 | 4 | Aag63982 Amino aci |
| 21 | 1819.5 | 67.2 | 549 | 5 | Aag63985 Amino aci |
| 22 | 1819.5 | 67.2 | 549 | 5 | Aae23291 Mouse nec |
| 23 | 1794 | 66.3 | 559 | 4 | Aam40929 Human pol |
| 24 | 1235 | 45.6 | 267 | 4 | Aam93536 Human pol |
| 25 | 1235 | 45.6 | 267 | 8 | Adl31248 Human pro |

| | | | | | | |
|----|-------|------|-----|---|----------|-----------|
| 26 | 642.5 | 23.7 | 305 | 5 | ADR41425 | Human CD- |
| 27 | 588 | 21.7 | 514 | 6 | ABJ20237 | Human IG |
| 28 | 588 | 21.7 | 517 | 3 | AAy32390 | Herpesvir |
| 29 | 588 | 21.7 | 517 | 5 | AAE23294 | Human nec |
| 30 | 587.5 | 21.7 | 458 | 5 | AAE23295 | Human nec |
| 31 | 565.5 | 20.9 | 518 | 5 | ABG77170 | Prostate |
| 32 | 551.5 | 20.4 | 578 | 8 | ADP03592 | Infection |
| 33 | 543 | 20.1 | 580 | 8 | ADO47877 | AlphaHer |
| 34 | 543 | 20.1 | 581 | 8 | ADP03590 | Infection |
| 35 | 540 | 19.9 | 530 | 8 | ADJ76222 | Marker ge |
| 36 | 538.5 | 19.9 | 485 | 8 | ADK83283 | Human 191 |
| 37 | 538.5 | 19.9 | 485 | 8 | ADK83298 | Human 191 |
| 38 | 538.5 | 19.9 | 485 | 8 | ADK83184 | Human 191 |
| 39 | 538.5 | 19.9 | 485 | 8 | ADK83202 | Human 191 |
| 40 | 538.5 | 19.9 | 485 | 8 | ADK83285 | Human 191 |
| 41 | 538.5 | 19.9 | 497 | 5 | AAE23303 | Human nec |
| 42 | 537 | 19.8 | 498 | 5 | AAE23305 | Human nec |
| 43 | 530.5 | 19.6 | 352 | 8 | ABM83397 | Human dia |
| 44 | 530.5 | 19.6 | 353 | 8 | ABM83396 | Human dia |
| 45 | 530.5 | 19.6 | 353 | 8 | ABM83395 | Human dia |

ALIGNMENTS

RESULT 1

AAE23286
ID AAE23286 standard; protein; 510 AA.

XX AC AAE23286;

XX AC AAE23286;

DT 27-AUG-2002 (first entry)

XX Human nectin-3beta protein.

DE Human nectin-3beta protein.

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW odema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

PA (IMV) IMMUNEX CORP.
 XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 XX WPI; 2002-426103/45.
 DR N-PSDB; AAD37445.
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT Glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX Claim 1; Page 98-99; 141pp; English.
 XX The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is human nectin-3beta protein.
 CC Human nectin-3beta gene is located on chromosome 3
 XX Sequence 510 AA;
 SQ
 Query Match 100.0%; Score 2707; DB 5; Length 510;
 Best Local Similarity 100.0%; Pred. No. 7.8e-213; Mismatches 0; Gaps 0;
 Matches 510; Conservative 0; Indels 0;
 QY 1 MARTLRSPCLPCGGKQAQLSSASLLGALLQPTPPPLLLLPPLLLFSLRCLGALGPI 60
 DB 1 MARTLRSPCLPCGGKQAQLSSASLLGALLQPTPPPLLLLPPLLLFSLRCLGALGPI 60
 QY 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQVQGR 120
 DB 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQVQGR 120
 QY 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTFPNETATIIISQYKLPPTTFAR 240
 DB 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTFPNETATIIISQYKLPPTTFAR 240
 QY 241 GRRITCVKHPALKEKDIRYSFILDIQVAPEVSVTGYDGNWFGKGNLKNADANPPPF 300
 DB 241 GRRITCVKHPALKEKDIRYSFILDIQVAPEVSVTGYDGNWFGKGNLKNADANPPPF 300
 QY 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVPF 360
 DB 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVPF 360
 QY 361 KQTSIAVAGAVIGAVLALFIIAIFVTLVLPKRPSPYLDKVIDLPPTHKPPPLYEERS 420
 DB 361 KQTSIAVAGAVIGAVLALFIIAIFVTLVLPKRPSPYLDKVIDLPPTHKPPPLYEERS 420
 QY 421 PPLPKQLFQPEHLPLQTFQKEREVGNLQHNGLNSRSFDYEDENPVGEDIQOMYPLYN 480
 DB 421 PPLPKQLFQPEHLPLQTFQKEREVGNLQHNGLNSRSFDYEDENPVGEDIQOMYPLYN 480
 QY 481 QMCYQDRSPGKHQNNDPKRVYIDPREHYV 510

DB 481 QMCYQDRSPGKHQNNDPKRVYIDPREHYV 510
 RESULT 2
 AAE23285
 ID AAE23285 standard; protein; 510 AA.
 XX AAE23285;
 AC AAE23285;
 XX 29-AUG-2003 (revised)
 DT 27-AUG-2002 (first entry)
 XX Mouse nectin-3-human nectin-3beta fusion protein.
 XX Human, nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
 XX Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 PH Key Location/Qualifiers
 FT Region 1..6 /note= "Mouse nectin-3 pprotein"
 FT Region 7..510 /note= "Human nectin-3beta protein"
 FT Region 7..510 /note= "Human nectin-3beta protein"
 PN W0200228502-A2.
 XX 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US031392.
 XX 05-OCT-2000; 2000US-0238557P.
 XX (IMV) IMMUNEX CORP.
 XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 WPI; 2002-426103/45.
 N-PSDB; AAD37444.
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT Glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX Claim 1; Page 94-95; 141pp; English.
 XX The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein encoding 6
 CC amino acids from mouse nectin-3 protein and the rest form human nectin-
 CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.


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Db      481 RSPGKHQNNDKRVVIDPREHYV 504
RESULT 4
AAG63983
ID      AAG63983 standard; protein; 510 AA.
XX
AC      AAG63983;
XX
XX      26-NOV-2001 (first entry)
XX
DE      Amino acid sequence of murine nectin-3.
XX
XX      Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
XX
OS      Mus sp.
XX
PN      WO200166736-A1.
XX
PD      13-SEP-2001.
XX
XX      09-MAR-2001; 2001WO-JP001871.
XX
PF      09-MAR-2000; 2000JP-00065595.
XX
PR      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PA      (TAKA/) TAKAHASHI K.
XX
XX      Takahashi K, Takai Y, Nakanishi H, Sato K;
XX
XX      WPI; 2001-570771/64.
XX
DR      N-PSDB; AAH78180.
XX
XX      New protein family for diagnosing and treating tumor infiltration and
XX      metastasis comprises the mouse nectin-3 protein families and
XX      corresponding antibodies.
XX
XX      Claim 2; Page 45-48; 64pp; Japanese.
XX
XX      The present sequence represents a murine nectin-3 polypeptide. Nectin-3
XX      is an immunoglobulin-like cell adhesion molecule that shows homophilic
XX      and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
XX      polynucleotides are useful for investigating the mechanisms of cell
XX      adhesion, infiltration and metastasis of cancer cells, the diagnosis of
XX      malignancies of various cancers, and the development of methods for the
XX      treatment and prevention of cancer
XX
XX      Sequence 510 AA;
XX
Query Match      88.2%; Score 2388; DB 4; Length 510;
Best Local Similarity 88.8%; Pred. No. 1.le-186;
Matches 454; Conservative 22; Mismatches 33; Indels 2; Gaps 2;
QY      1 MARTLRSPICPGGKQALSASLLGAGLLLOPPTPPPLLLLPFLLSRLCAGAPI 60
Db      1 MARTPGAPICPGGKQALSAPFAAGLLLPAPTTPPLLLLPFLLSRLCAGAGSI 60
QY      61 IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFSGYQGR 120
Db      61 IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHPQYGFSGYQGR 120
QY      121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTTVTLVEPTVSLIKGPD 180
Db      121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTTVTLVEPTVSLIKGPD 180
QY      181 LIDGGNETVAACITAAATGKPAHIDWEGDGLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db      181 LIDGGNETVAACVAAATGKPAQIDWEGDGLGEMESTTSPNETATIVSQIKLPPTFRAR 240
QY      241 GRRITCVVKKHAPALEKDIRYSFILDIOYAPEVSVTVGYDGNWFGVGRKGNLKNADANPPPF 300
Db      241 GRRITCVVKKHAPALEKDIRYSFILDIOYAPEVSVTVGYDGNWFGVGRKGNLKNADANPPPF 300
QY      301 KSWMSRLDQWPDGGLASDNTLHFVHLPTFNYSVVYICKVNTSLGORSQDKVIYISDVVPF 360
Db      301 KSWMSRLDQWPDGGLASDNTLHFVHLPTFNYSVVYICKVNTSLGORSQDKVIYISDVPL 360
QY      361 KOTSSIAVAGAVIGAVLALFIIAIFVTLLTPRKRPSPYLDKVIDLPPTHKPPPLYEERS 420
Db      361 TOTSSIAVAGAVIGAVLALFIITVFTVLLTPRKRPSPYLDKVIDLPPTHKPPPLYEERI 420
QY      421 PPLPKDLF-QPEHLPLQTFKREVEGNLOHNSGLNSRFDYEDENPVGSDGLOQMPLY 479
Db      421 PSLPQKDLGLQTEHLPLQTFKKEGAGGLQPSNGPISRFRDYEDESTMOBDSGTQRMCPY 480
QY      480 NMCVQDRSPGKHQNNDKRVVIDPREHYV 510
Db      481 SQMCHQDRSPRQHHPRN-PERLYINPREHYV 510
XX
RESULT 5
AAE23292
ID      AAE23292 standard; protein; 510 AA.
XX
AC      AAE23292;
XX
XX      27-AUG-2002 (first entry)
XX
DE      Mouse nectin-3beta protein.
XX
XX      Mouse; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
XX      paracellular transport disorder; kidney; diabetic retinopathy; allergy;
XX      allograft rejection; metastasis; restenosis; inflammatory bowel disease;
XX      oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
XX      stroke; tumour; cancer; herpesvirus infection; asthma.
XX
OS      Mus musculus.
XX
XX      WO200228902-A2.
XX
XX      11-APR-2002.
XX
XX      05-OCT-2001; 2001WO-US031392.
XX
XX      05-OCT-2000; 2000US-0238557P.
XX
XX      (IMMV ) IMMUNEX CORP.
XX
XX      Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX      WPI; 2002-426103/45.
XX
XX      Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX      useful for treating or preventing heart failure, malaria,
XX      glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX      sepsis, stroke.
XX
XX      Disclosure; Page 109-110; 141pp; English.
XX
XX      The invention relates to a substantially purified nectin3alpha, beta,
XX      gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX      Nectin DNA and protein are useful for treating a disease associated with
XX      cell adhesion activity, adherens junction formation activity, epithelial
XX      or endothelial barrier function activity, endothelial proliferation or
XX      migration activity, viral polypeptide binding activity. The epithelial or
XX      endothelial barrier function disorder which is treated by the above
XX      mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX      asthma, allergy, allograft rejection, metastasis of cancer cells,
XX      paracellular transport disorders such as magnesium transport defects in
XX      the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX      inhibiting angiogenesis in a mammal and treating endothelial migration,
XX      ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX      stroke, restenosis, tumour growth and treating herpesvirus infection.
XX      Nectin is also useful for modulating proliferation or migration of an
XX      endothelial cell, an epithelial cell or a smooth muscle cell (vascul

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| | | |
|----------|---|--|
| CC | smooth muscle cell). The present sequence is mouse nectin-3beta protein | |
| XX | | |
| SQ | Sequence 510 AA; | |
| | Query Match | 88.2%; Score 2388; DB 5; Length 510; |
| | Best Local Similarity | 88.8%; Pred. No. 1.1e-186; |
| | Matches 454; Conservative | 22; Mismatches 33; Indels 2; Gaps 2; |
| QY | 1 | MARTLRPSPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLLPPLLLFRLRCGALAGPI 60 |
| DB | 1 | MARTPGAPLCPGGGKAQLSAPPAAGLLLPAPTPTPLLLLLLPLLLFRLRCGALAGSI 60 |
| QY | 61 | IVPHVTVAVGKNVSLKCLLEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120 |
| DB | 61 | IVPHVTVAVGKNVSLKCLLEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVOGDYQGR 120 |
| QY | 121 | VLFNYSLNDAITTLHNIGFSDSGKYCKAVTFLGNAQSSSTTVTLVLEPTVSLIKGPD 180 |
| DB | 121 | VLFNYSLNDAITTLHNIGFSDSGKYCKAVTFLGNAQSSSTTVTLVLEPTVSLIKGPD 180 |
| QY | 181 | LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTFAR 240 |
| DB | 181 | LIDGNETVAAVCVAATGKPAQIDWEGDLGEMESTTSPNETATIVSQYKLPPTTFAR 240 |
| QY | 241 | GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGYNLKNADANPPFF 300 |
| DB | 241 | GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGYNLKNADANPPFF 300 |
| QY | 301 | KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVVICKVTNSLQORSQDKVIIVSDVPF 360 |
| DB | 301 | KSVWSRLDGGWPDGLLASDNTLHFVHPLTFNYSGVVICKVTNSLQORSQDKVIIVSDIPL 360 |
| QY | 361 | KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSEYLDKVIDLDPPTHKPPPEERS 420 |
| DB | 361 | TQTSSIAVAGAVIGAVLAFIITVFTVLLTPRKRPSEYLDKVIDLDPPTHKPPPEERI 420 |
| QY | 421 | PSLPQKDLF-OPEHLPLQTOFKEREVGNLQNSRSEFDYEDENPVGEGDQOMVPLY 479 |
| DB | 421 | PSLPQKDLGQTEHLPLQTOFKKGAGGLQPSNGPISRRFDYEDESTMQEDGTQMCPLY 480 |
| QY | 480 | NOMCYQDRSPGKHQNNQDKRVYIDPREHYV 510 |
| DB | 481 | SQMCHQDRSPQHPRN-PERLYINPREHYV 510 |
| RESULT 6 | | |
| AAE23299 | | |
| ID | AAE23299 standard; protein; 437 AA. | |
| XX | AAE23299; | |
| XX | | |
| AC | | |
| DT | 27-AUG-2002 (first entry) | |
| XX | | |
| DE | Human nectin-3gamma protein. | |
| XX | | |
| KW | Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis; | |
| KW | paracellular transport disorder; kidney; diabetic retinopathy; allergy; | |
| KW | allograft rejection; metastasis; restenosis; inflammatory bowel disease; | |
| KW | oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; | |
| KW | stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | W0200228902-A2. | |
| XX | | |
| PD | 11-APR-2002. | |
| XX | | |
| PF | 05-OCT-2001; 2001WO-US031392. | |
| XX | | |
| PR | 05-OCT-2000; 2000US-0238557P. | |
| XX | | |
| XX | (IMMV) IMMUNEX CORP. | |
| XX | | |


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Db 1 MARTPGAPLPCGGKQAQLSSAFPPAAGLLLPAPTPPPLLLLLPLLLFRLCGALAGSI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGYQGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSGVDYQGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDIP 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 KOTSSIAVAGAVICAVLAFIATFVTLTPRKRPSYLDKVIDLPTHKPPPLYEERS 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 TQTSSIAVAGAVICAVLAFIATFVTLTPRKRPSYLDKVIDLPTHKPPPLYEBERI 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 PPLPKDIL 428
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 PSLPKDIL 428
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
AAE23283
ID AAE23283 standard; protein; 549 AA.
AC AAE23283;
XX
XX 27-AUG-2002 (first entry)
DT
DE Human nectin-3alpha protein.
XX
XX Human, nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 73
FT /note= "N-glycosylated"
FT Domain 74..152
FT /note= "Extracellular Ig domain"
FT Modified-site 83
FT /note= "N-glycosylated"
FT Modified-site 125
FT /note= "N-glycosylated"
FT Modified-site 186
FT /note= "N-glycosylated"
FT Domain 189..250
FT /note= "Extracellular Ig domain"
FT Modified-site 222
FT /note= "N-glycosylated"
FT Domain 287..342
FT /note= "Extracellular Ig domain"
FT Modified-site 331
FT /note= "N-glycosylated"
FT Domain 405..424
FT /note= "Transmembrane domain"
FT Domain 425..549
FT /note= "C-terminal domain"
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```
XX PN W0200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV ) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37442.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX Claim 1; Page 89-91; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,
XX proliferation or angiogenic condition of a tissue or a subject, such as
XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX stroke, restenosis, tumour growth and treating herpesvirus infection.
XX Nectin is also useful for modulating proliferation or migration of an
XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
XX smooth muscle cell). The present sequence is human nectin-3alpha DNA.
XX Human nectin-3alpha gene is located on chromosome 3
XX
XX Sequence 549 AA;
XX
XX Query Match 70.9%; Score 1920.5; DB 5; Length 549;
XX Best Local Similarity 67.9%; Pred. No. 2.4e-148;
XX Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
```

```
Qy 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLLFRLCGALAGPI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLLPPTPPPLLLLLFRLCGALAGPI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGYQGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IVEPHVTAVGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGYQGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP- 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPT 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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360 -----FKOTSSIAVAGAVIGAVLALFIIA 383
 361 TTTLTQTIQWHPSTADIEDLATEPKLPFPPLSLTATIKDDTIATIIASVVGALFIVLVS 420
 384 IFVTVLLTPRK--RPSYLDKVIDLPPTHK-----PPPLYERSPPPLP 424
 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQBELDSYPDSVKKENKPV- 478
 425 QKDLFOPEHL--PLOTQPKEREVGNLQHSNLSRSPDYEDENPVGDGIGQQWYPLYNQM 482
 479 -NNLRKDYLEBEKTOQ-----NNVENLNR-ERPMDYEDLKMGMKFVSD----- 523
 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
 524 -----EHYDENEDDLVSHVDGVSISRREWTV 549

RESULT 10
 ABJ20222
 ID ABJ20222 standard; protein; 549 AA.
 AC ABJ20222;
 XX
 XX 13-AUG-2003 (first entry)
 DT
 XX
 XX Human IG gene related protein SEQ ID No 45.
 XX
 XX Breast cancer; p53 pathway modulating agent; IG; colon cancer;
 KW kidney cancer; lung cancer; ovary cancer; human.
 KW
 XX Homo sapiens.
 OS
 XX WO200299040-A2.
 PN
 XX 12-DEC-2002.
 PD
 XX
 XX 03-JUN-2002; 2002WO-US017313.
 XX
 XX 05-JUN-2001; 2001US-0296076P.
 PR
 PR 10-OCT-2001; 2001US-0328605P.
 PR
 PR 22-OCT-2001; 2001US-0338733P.
 PR
 PR 15-FEB-2002; 2002US-0357253P.
 PR
 PR 15-FEB-2002; 2002US-0357600P.
 XX
 XX (EXEL-) EXELIXIS INC.
 XX
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI Lioubin MN;
 PI
 XX WPI; 2003-148660/14.
 XX
 XX Identifying a candidate p53 pathway modulators that are useful as targets
 PT for therapeutics or for diagnosing cancers associated with defective p53
 PT function, by providing an assay system having a purified IG polypeptide
 PT or nucleic acid.
 XX
 XX Claim 13; Page 206-209; 248pp; English.
 PS
 XX The invention relates to a novel method for identifying a candidate p53
 CC pathway modulating agent. The method comprises providing an assay system
 CC having a purified IG polypeptide or nucleic acid, or their functionally
 CC active fragment or derivative. The method is useful for identifying
 CC modulators of the p53 pathway, particularly for identifying agents for
 CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
 CC cancer or cancer of the ovary) associated with defective p53 function.
 CC The identified modulators are useful as targets for novel therapeutics.
 CC The method is also useful for diagnosing disorders associated with
 CC defective p53 function. The IG proteins or nucleic acids are useful as
 CC modifiers of the p53 pathway, and as therapeutic targets for disorders
 CC associated with defective p53 function. This sequence represents a human
 CC protein relating to the human IG genes used in the assay for identifying
 CC modulators of the p53 pathway of the invention
 CC

SQ Sequence 549 AA;
 Query Match 70.9%; Score 1920.5; DB 6; Length 549;
 Best Local Similarity 67.9%; Pred. No. 2.4e-148;
 Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

QY 1 MARTLRPSPLCPGCGKAQLSSASLLGAGLLLOPPTPPPLLLFPPLLSRLCGALAGPI 60
 Db 1 MARTLRPSPLCPGCGKAQLSSASLLGAGLLLOPPTPPPLLLFPPLLSRLCGALAGPI 60
 QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPOGFSGVQGYQR 120
 Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPOGFSGVQGYQR 120
 QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAOSSTTVTVLVPTVSLIKGPD 180
 Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAOSSTTVTVLVPTVSLIKGPD 180
 QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQKLFPTFRAR 240
 Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQKLFPTFRAR 240
 QY 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGDGNWFGVGRKGNLKNADANPPPF 300
 Db 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGDGNWFGVGRKGNLKNADANPPPF 300
 QY 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVYICKVNSLQORSQDKVIYISDVP- 359
 Db 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVYICKVNSLQORSQDKVIYISDVP 360
 QY 360 -----FKOTSSIAVAGAVIGAVLALFIIA 383
 Db 361 TTTLTQTIQWHPSTADIEDLATEPKLPFPPLSLTATIKDDTIATIIASVVGALFIVLVS 420
 QY 384 IFVTVLLTPRK--RPSYLDKVIDLPPTHK-----PPPLYERSPPPLP 424
 Db 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQBELDSYPDSVKKENKPV- 478
 QY 425 QKDLFOPEHL--PLOTQPKEREVGNLQHSNLSRSPDYEDENPVGDGIGQQWYPLYNQM 482
 Db 479 -NNLRKDYLEBEKTOQ-----NNVENLNR-ERPMDYEDLKMGMKFVSD----- 523
 QY 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
 Db 524 -----EHYDENEDDLVSHVDGVSISRREWTV 549

RESULT 11
 ADR66369
 ID ADR66369 standard; protein; 549 AA.
 XX
 AC ADR66369;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Human prostatic carcinoma derived protein SEQ ID 223 #2.
 XX
 XX human; cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis.
 XX
 XX Homo sapiens.
 XX WO2004076614-A2.
 XX
 XX 10-SEP-2004.
 PD
 XX 22-FEB-2004; 2004WO-DE000433.
 XX
 XX 27-FEB-2003; 2003DE-01009985.
 PR
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 XX (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA

CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
XX Sequence 549 AA;

Query Match 70.9%; Score 1920.5; DB 8; Length 549;
Best Local Similarity 67.9%; Pred. No. 2.4e-148;
Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
Qy 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLFRRLGALAGPI 60
Db 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLFRRLGALAGPI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAHHPOYGFVSQYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAHHPOYGFVSQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMSTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMSTTSPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP- 359
Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP 360
Qy 360 -----FKQTSSIAVAGAVI GAVLALFIIA 383
Db 361 TTTLOPTIQWHPSTADIEDLATEPKLPFLPLSTLATIKDITATIIASVVGALFVLVS 420
Qy 384 IFVTVLITPRKK--RPSYLDKVIDLPETHK-----PPPLYEERSPLP 424
Db 421 VLAGIFCYRRRTFRGDFYFAKNY-IPPSDWOKESQIDVLQODELSDYSDSKKNKNPV- 478
Qy 425 QKDLFQPEHL--PLQTOFKEREVENLQHSNLSRSPDYEDENPVNGBDGIQOMYPLYNQM 482
Db 479 -NNLRKDYLEEPEKTQW-----NNVENLRF-ERPMDYIEDLKQGMKFFVSD----- 523
Qy 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510
Db 524 -----EHYDENEDDLVSHVDSGVSISRREWYV 549
RESULT 13
AAE23288
ID AAE23288 standard; protein; 595 AA.
XX
XX AAE23288;

XX
XX 27-AUG-2002 (first entry)
DE Human nectin-3beta-IgG1Fc region fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; testenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
XX WO200228902-A2.
XX
PD 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX
XX Claim 9; Page 102-104; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adhesion junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,
XX proliferation or angiogenic condition of a tissue or a subject, such as
XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX stroke, restenosis, tumour growth and treating herpesvirus infection.
XX Nectin is also useful for modulating proliferation or migration of an
XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
XX smooth muscle cell). The present sequence is a fusion protein containing
XX human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
XX Sequence 595 AA;
Query Match 70.7%; Score 1914; DB 5; Length 595;
Best Local Similarity 86.3%; Pred. No. 9.3e-148;
Matches 373; Conservative 3; Mismatches 18; Indels 38; Gaps 2;
Qy 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLFRRLGALAGPI 60
Db 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLFRRLGALAGPI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAHHPOYGFVSQYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAHHPOYGFVSQYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTFAR 240
Qy 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSUTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSUTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSVGVIKVTNSLGQSDOKVYIISDVPP 360
Db 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSVGVIKVTNSLGQSDOKVYIISDVPP 360
Qy 361 KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRKFSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KQTSSRS-----CDK-----THCPCCPAPEA 382
Qy 421 PPLPQKDLQPE 432
Db 383 EGAPSVLEFPK 394

RESULT 14
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX AC AAE23290;
XX DT 27-AUG-2002 (first entry)
XX DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; resclerosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX OS Homo sapiens.
XX OS Unidentified.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX FT Region 1..365
XX FT /note= "Human nectin-3alpha protein"
XX FT Region 366..381
XX FT /note= "FLAG peptide"
XX FT Region 382..387
XX FT /note= "PolyHis tag"
XX PN WO200228902-A2.
XX PD 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US031392.
XX PR 05-OCT-2000; 2000US-0238557P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX DR Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX FT useful for treating or preventing heart failure, malaria,
XX PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX FT sepsis, stroke.
XX PS Claim 9; Page 105-107; 141pp; English.
XX CC The invention relates to a substantially purified nectin3alpha, beta,

CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, resclerosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta-
CC FLAGpolyHis fusion protein
XX SQ Sequence 387 AA;

Query Match 70.6%; Score 1912; DB 5; Length 387;
Best Local Similarity 99.5%; Pred. No. 7.5e-148;
Matches 363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGGGKAQSSASLLGAGLLQLQPTPPPLLLLPLLLFRLCGALAGPI 60
Db 1 MARTPGSPPLCPGGGKAQSSASLLGAGLLQLQPTPPPLLLLPLLLFRLCGALAGPI 60
Qy 61 IVEPHYTVAVWKNVSLKCLIEVNETTIOISWEKHGKSSQTVAVHHPOYGSVOGEYQGR 120
Db 61 IVEPHYTVAVWKNVSLKCLIEVNETTIOISWEKHGKSSQTVAVHHPOYGSVOGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTFAR 240
Qy 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSUTGYDGNWFGVGRKGNLKNADANPPPF 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOVAPEVSUTGYDGNWFGVGRKGNLKNADANPPPF 300
Qy 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSVGVIKVTNSLGQSDOKVYIISDVPP 360
Db 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSVGVIKVTNSLGQSDOKVYIISDVPP 360
Qy 361 KQTSS 365
Db 361 KQTSS 365

RESULT 15
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX AC AAE23282;
XX DT 29-AUG-2003 (revised)
XX DT 27-AUG-2002 (first entry)
XX DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; resclerosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
XX KW chromosome 3.
XX OS Homo sapiens.

OS Mus musculus.
 XX Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Region 1..7
 FT /note= "Mouse nectin-3 protein"
 FT Region 8..549
 FT /note= "Human nectin-3alpha protein"
 XX
 PN W0200228902-A2.
 XX
 XX
 PD 11-APR-2002.
 XX
 XX 05-OCT-2001; 2001WO-US031392.
 XX
 XX 05-OCT-2000; 2000US-0238557P.
 XX
 XX (IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 XX WPI; 2002-426103/45.
 DR N-PSDB; AAD37441.
 XX
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT Glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX
 XX Claim 1; Page 80-82; 141pp; English.
 XX
 CC The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein containing
 CC mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
 CC alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 549 AA;
 Query Match 70.4%; Score 1906.5; DB 5; Length 549;
 Best Local Similarity 67.6%; Pred. No. 3.4e-147;
 Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;
 QY 1 MARTLRPSPLCPGGGKQAQLSSASLLGAGLLLOPPTPPPLLLPPLLLPRLGALAGPI 60
 DB 1 MARTPGSPPLCPGGGKQAQLSSASLLGAGLLLOPPTPPPLLLPPLLLPRLGALAGPI 60
 QY 61 IVEPHVTVAVMGKNSVLSKCLIEVNETITQISWEKINGKSSQTFVAVHHPQYGFSGVQYQGR 120
 DB 61 IVEPHVTVAVMGKNSVLSKCLIEVNETITQISWEKINGKSSQTFVAVHHPQYGFSGVQYQGR 120
 QY 121 VLFKNYSINDATITLHNIGSDSGKYICKAVTFPLGNAQSSSTTVTLVPEVTSVLIKGPD 180
 DB 121 VLFKNYSINDATITLHNIGSDSGKYICKAVTFPLGNAQSSSTTVTLVPEVTSVLIKGPD 180
 QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTRFAR 240

DB 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTRFAR 240
 QY 241 GRRITCVVGHPALEKDIRYSFILDIOYAPEVSVTYDGNWFGVGRKGVNLCNADANPPPF 300
 DB 241 GRRITCVVGHPALEKDIRYSFILDIOYAPEVSVTYDGNWFGVGRKGVNLCNADANPPPF 300
 QY 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVNTSLGQSDQKVYIISDVP- 359
 DB 301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVNTSLGQSDQKVYIISDVP 360
 QY 360 -----FKQTSIAVAGAVIGAVLALFIIA 383
 DB 361 TTTLQPTIQMHPSTADIEDLATEPKKLPPLPLATIKDDTIATIIASVVGALFVLVS 420
 QY 384 IFVTVLLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPPPLP 424
 DB 421 VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQDDELDSYDPSVKKENKPV- 478
 QY 425 QKDLFOPEHL--PLOTQFKEREVGNLHNSRSDFYEDENPNVGEDGIQQWYPLYNQ 482
 DB 479 -NNLRKYDLEBEKTKQW-----NNVENLNR-ERPMDIYEDLKMGKMFVSD----- 523
 QY 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510
 DB 524 -----EHDYDENEEDLVSHVDGSGVISRREWTV 549
 Search completed: October 6, 2005, 09:51:36
 Job time : 86.2348 secs

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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:42:42 ; Search time 16.7671 Seconds
(without alignments)
2926.593 Million cell updates/sec

Title: US-09-972-268-12
Perfect score: 2707
Sequence: 1 MARTLRSPICPGGKAQLS.....KHQNNDPKRVYIDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 1173.5 | 43.4 | 407 | 2 T08732 | hypothetical prote |
| 2 | 565.5 | 20.9 | 518 | 2 JC4024 | poliovirus recepto |
| 3 | 540 | 19.9 | 530 | 2 A53437 | poliovirus recepto |
| 4 | 527 | 19.5 | 538 | 2 T68093 | PRR2 delta - human |
| 5 | 467 | 17.3 | 467 | 1 HLMS23 | poliovirus recepto |
| 6 | 455 | 16.8 | 478 | 2 I53960 | PRR2 alpha - human |
| 7 | 418 | 15.4 | 392 | 2 B44194 | poliovirus recepto |
| 8 | 418 | 15.4 | 417 | 2 A44194 | poliovirus recepto |
| 9 | 402 | 14.9 | 392 | 1 RWHUPD | poliovirus recepto |
| 10 | 402 | 14.9 | 417 | 1 RWHUPA | poliovirus recepto |
| 11 | 326.5 | 12.1 | 416 | 2 A54017 | colon carcinoma-as |
| 12 | 229.5 | 8.5 | 764 | 2 A49448 | irregular chiasm C |
| 13 | 205.5 | 7.6 | 4391 | 2 A38096 | perlecan precursor |
| 14 | 196.5 | 7.3 | 5175 | 2 T20932 | hypothetical prote |
| 15 | 196.5 | 7.3 | 5198 | 2 T43290 | hemacentin precurs |
| 16 | 187.5 | 6.9 | 274 | 2 A47639 | OX-2 membrane glyco |
| 17 | 181.5 | 6.7 | 1896 | 2 T08851 | Down syndrome cell |
| 18 | 178.5 | 6.6 | 3707 | 2 J18252 | heparan sulfate pr |
| 19 | 178 | 6.6 | 588 | 2 JH0506 | adhesion molecule |
| 20 | 178 | 6.6 | 588 | 2 A45254 | surface glycoprote |
| 21 | 177.5 | 6.6 | 853 | 1 TJB0NC | neural cell adhesi |
| 22 | 177 | 6.5 | 626 | 1 A61084 | myelin-associated |
| 23 | 177 | 6.5 | 637 | 2 B33785 | myelin-associated |
| 24 | 176 | 6.5 | 7962 | 2 I38346 | elastic titin - hu |
| 25 | 175 | 6.5 | 582 | 1 BNRT3S | myelin-associated |
| 26 | 175 | 6.5 | 626 | 1 BNRT3 | myelin-associated |
| 27 | 174 | 6.4 | 1091 | 2 A58532 | glial cell membran |
| 28 | 170.5 | 6.3 | 365 | 2 JC7780 | coxsackie- and ade |
| 29 | 164.5 | 6.1 | 847 | 2 JH0371 | B-cell adhesion pr |

| | | | | | |
|----|-------|-----|------|----------|---------------------|
| 30 | 162.5 | 6.0 | 278 | 1 TDRTOX | OX-2 membrane glyco |
| 31 | 162.5 | 6.0 | 858 | 1 LJRTNC | neural cell adhesi |
| 32 | 162 | 6.0 | 587 | 1 JH0464 | DM-GRASP precursor |
| 33 | 162 | 6.0 | 761 | 1 IJHUNG | neural cell adhesi |
| 34 | 162 | 6.0 | 765 | 2 C42632 | cell adhesion mole |
| 35 | 162 | 6.0 | 812 | 2 B42632 | cell adhesion mole |
| 36 | 162 | 6.0 | 932 | 2 A42632 | cell adhesion mole |
| 37 | 161.5 | 6.0 | 739 | 2 JN0581 | vascular cell adhe |
| 38 | 160.5 | 5.9 | 702 | 2 A36319 | carcinoembryonic a |
| 39 | 160 | 5.9 | 725 | 1 IJMSNG | neural cell adhesi |
| 40 | 157 | 5.8 | 509 | 2 JC5288 | SHP substrate-1 pr |
| 41 | 157 | 5.8 | 1091 | 1 IJCHNL | neural cell adhesi |
| 42 | 156 | 5.8 | 646 | 2 I38049 | cell surface glyco |
| 43 | 155 | 5.7 | 513 | 2 JC5289 | SHP substrate-1 pr |
| 44 | 154 | 5.7 | 1612 | 2 T30805 | cuttl protein - mo |
| 45 | 153.5 | 5.7 | 1051 | 2 A39712 | kinase-like protei |

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKFzp566B0846.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08732

R/Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16474

A/Accession: T08732

A/Molecule type: mRNA

A/Residues: 1-407 <OPT>

A/Cross-references: UNIPROT:Q9Y412; EMBL:AL050071

A/Experimental source: fetal kidney; clone DKFzp566B0846

C/Genetics:

A/Note: DKFzp566B0846.1

Query Match 43.4%; Score 1173.5; DB 2; Length 407;
Best Local Similarity 62.8%; Pred. No. 1e-78;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

| | | | |
|----|-----|---|-----|
| Qy | 143 | SGYICKAVTFPIGNAQSSTTVLVEPTVSLIKGPDSLIDGNETVAAICIAATGPVA | 202 |
| Db | 1 | SGRYICKAVTFPIGNAQSSTTVLVEPTVSLIKGPDSLIDGNETVAAICIAATGPVA | 60 |
| Qy | 203 | HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFPARGRRITCVVKHPALEKDIRYSFI | 262 |
| Db | 61 | HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFPARGRRITCVVKHPALEKDIRYSFI | 120 |
| Qy | 263 | LDIQAYEVSVTGYDGNWFVGRKGVNLKCNADANPPFPKSVWSRLDQGWPDGLASDNTL | 322 |
| Db | 121 | LDIQAYEVSVTGYDGNWFVGRKGVNLKCNADANPPFPKSVWSRLDQGWPDGLASDNTL | 180 |
| Qy | 323 | HFVHPLTFNYSGVYICKVTNSLQORSQKVIYISDVP----- | 359 |
| Db | 181 | HFVHPLTFNYSGVYICKVTNSLQORSQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT | 240 |
| Qy | 360 | -----FKQTSIAVAGAVIGAVLALFIATFVTVLLTPRKK--RESYLDKV | 403 |
| Db | 241 | EPKKLPPLSLATATIKDDTIATIIASVVGALFVLVSLAGIFCYRRRTFRGDYFAKN | 300 |
| Qy | 404 | IDLPPPTH-----KPPPLYEERSPPLPKDLFQPEHL--PLQTPQKEREVG | 446 |
| Db | 301 | Y-TPSPDMQESQIDVLQDELDPYPSVKENKPNVNNLRKDYLEPEKTTQW-----N | 354 |
| Qy | 447 | NLOHNSGLNSRSFYDENPNVG | 468 |
| Db | 355 | NVENLNRF-ERPMDYYEDLKMG | 375 |

RESULT 2

JC4024

poliovirus receptor-related protein precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C;Accession: J04024
 R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubh
 Gene 155, 261-265, 1995
 A;Title: Complementary DNA characterization and chromosomal localization of a human gene
 A;Reference number: J04024; MUID:95237621; PMID:7721102
 A;Accession: J04024
 A;Molecule type: mRNA
 A;Residues: 1-518 <LOP>
 A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
 C;Genetics:
 A;Gene: GDB:PVRR1
 A;Cross-references: GDB:583951
 A;Map position: 11q23-11q24
 C;Superfamily: poliovirus receptor; immunoglobulin homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F;356-379/Domain: transmembrane #status predicted <TM>
 F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.9%; Score 565.5; DB 2; Length 518;
 Best Local Similarity 29.0%; Pred. No. 7.8e-34;
 Matches 148; Conservative 85; Mismatches 171; Indels 107; Gaps 16;

QY 71 GKNVSLKCLIE--VNTTITQISWEKIHGKSSQTAVVHHPOYGFVSQGEYQGRVLPKNYS 127
 DB 44 GTDVLHCSFANPLSPVKITQVTWQKSTNGSKQNVAIYNPMSGVSLAPYRERVEFLRPS 103

QY 128 LNDATITLHNGSDSKYICKAVTFPLGNAQSSTTVTLVETVSLIKGPDSLIDG--- 184
 DB 104 FTDGTRLSLELEDEGVYICEFATFPFGNRESQNLNLTWAKPT-NWIEGTQAVLRKKG 162

QY 185 -GNETVAACIAATGKQVAHIDWE-----GDLGEMESTTSPNETATIIISOYKL 233
 DB 163 QDQKVLVATCISANGKPPSVVSWETRLKGEARVPGDSGT-----PMAPVTIVISEYRL 214

QY 234 PPTRFARGRRITCVVHPALEKDIRYFILDIOYAPESVTVGDNFVGRGKGNLKCNA 293
 DB 215 VPSREAHQSLACIVNYHM--DRFKESLTINVQYEPVETIEGFDGNWYLQRMVDVLTCKA 272

QY 294 DANPPPKFSWSRLDQWPGGLASDNTLHFVPLTFNYSQVYICKVNTSLGORSQDKVI 353
 DB 273 DANPPATPEYHTWTLNGLSLPKGVEAQNRITLFPKGIPNYSLAGTYICEATNPIDTRSGQVEV 332

QY 354 YISDVPPKQTS-----STAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLD 401
 DB 333 NITEFPYTPPPEHGRAGVPVTAIIGVAGSILLVIVVGIVVALRRRHFTKGDYST 392

QY 402 K-----VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSN 452
 DB 393 KKHVYNGYSKAGIPQH--PPMAQNLQYPPDSD--EKKAGPLGGS- 435

QY 453 GLNSRSFDYEDNPVGEDGQQM-----YPLYN-----QMCYQDRSPGKH 492
 DB 436 -----SYEBEEEEEGGGGERKVGPHKPYDEDAKRPYFTVDEAARQDGYGDRTLGYQ 490

QY 493 HQNNDRPV-----YIDPREHYV 510
 DB 491 Y---DPEQLDLAENMVNSQDGSFISKKEWYV 518

RESULT 3
 A53437
 poliovirus receptor mpvr - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A53437
 R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
 J. Biol. Chem. 269, 8431-8438, 1994
 A;Title: Amino acid residues on human poliovirus receptor involved in interaction with p

A;Reference number: A53437; MUID:94179228; PMID:8132569
 A;Accession: A53437
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-530 <AK>
 A;Cross-references: UNIPROT:P32507; GB:D26107; NID:g475017; PIDN:BA05103.1; PID:g825507
 A;Experimental source: C57/BL6, brain
 A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
 C;Superfamily: poliovirus receptor; immunoglobulin homology
 F;47-133/Domain: immunoglobulin homology <IMM>

Query Match 19.9%; Score 540; DB 2; Length 530;
 Best Local Similarity 28.8%; Pred. No. 6.1e-32;
 Matches 153; Conservative 85; Mismatches 214; Indels 80; Gaps 17;

QY 30 LIQPTPPPLLLLLLFPILLFSLRCLGALAGPIIVEPHVTAVWKNVSLKC--LLEVNETIT 87
 DB 6 VLPFSLSLPTLLPLLLLLLLOETGAQDVRVRLPEVGRGLGTVELPCHLLPPTTTERVS 65

QY 88 QISWEKIHGKSSQTAVVHHPOYGFVSQGEY--QGRVLF-----KNVSLNDATITLHNIG 139
 DB 66 QVTWQLDQ---TVVAAPHSFQVDPNPSQFSKDRLSFVRARPETWADLEDAFLAFLR 122

QY 140 FDSGKYICKAVTFPLGNAQSSTTVTLVVEP-----TVSLIKGPDSLIDGNETVAACI 194
 DB 123 VEDEGNYTCFATFPNGTRRGVTLRVIAQPNHAEAEQVETIGQSV-----AVARCV 175

QY 195 AATGKPAVIDHEGDLGEMESTTSPN---ETATIIISQYKLPPTRFARGRRITCVVKHP 251
 DB 176 STGGRPPARITWISSLGG-EAKDTQEPGIAQAGVTITISRYSLVPVGRADGVKVTCTVEHE 234

QY 252 ALEKDIRYFILDIOYAPESVTVGDNFVGRGKGNLKCNDANPPPKFSWSRLDQW 311
 DB 235 SFEELPVLTVLSRVTPPEVSGYDDNWLGRSEAILICDVRSNEPTDYDSTTSQGVF 294

QY 312 PDGLLASDNTLHFVPLTFNYSQVYICKVNTSLGORSQDKVIYISDVPPKQTSIAVAGA 371
 DB 295 PASAVAQSQL-LVHSDVRMVTTFICTATNAVGTGRAEQVILVRESP--STAGAGATGG 351

QY 372 VIGAVLALFI-TAIFVTVLLTPRKPSYL-----DKVIDLPPTHKPP-PLYEERSPPL 423
 DB 352 IIGGIIAIIATAVAGTGILICRQKQRLQAADDEEELEGPPSYKYPPTPKALEPEM 411

QY 424 PQK--DLFQPEHLPLQTF-----KREVGNLQHSNGLN----- 455
 DB 412 PSQFTLGLASEHSPVKIPYFDAGVSCADQEMPRYHELPTLEERSGPLLGLATGLGPSLLV 471

QY 456 -----SRSFDYEDNPVGEDGIIQWYPLYNQMCYQDRSPGKHQNNND 497
 DB 472 PPGPNVVEGVSLSLEDEDEEDFLDKINPIYDALSYF--SPSDSYQSKD 521

RESULT 4
 I68093
 PR2 delta - human
 C;Species: Homo sapiens (man)
 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159, 267-272, 1995
 A;Title: The human PR2 gene, related to the human poliovirus receptor gene (PVR), is the
 A;Reference number: I53960; MUID:95347610; PMID:7622062
 A;Accession: I68093
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-538 <RES>
 A;Cross-references: UNIPROT:Q92692; GB:S79172; NID:g1042204; PID:g1042205
 C;Genetics:
 A;Gene: PR2delta
 C;Superfamily: poliovirus receptor; immunoglobulin homology
 F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 19.5%; Score 527; DB 2; Length 538;

```

Best Local Similarity 27.3%; Pred. No. 5.6e-31;
Matches 151; Conservative 94; Mismatches 206; Indels 102; Gaps 21;

Qy 33 PPTPPPLLLPPLLLPRL- CGALAGPIIIEPHVHTAVWGNVSLKCLII---EYNETITQ 88
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 PPTP-----LLWPLLLLLLLTGAQDVRVQVLPVGRGLGGTVELPCHLLPPVGLYISL 67

Qy 89 ISWEKIHGKSS-QTVAVHHPOYGSVOGEYQ--RVLF-----KNYSLNDATITL 135
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 VTWRDPAPANHQAFAHFKMGSPFPSPKPGSRLSFVSAKQSTGQDTEAELQDATAL 127

Qy 136 HNIQFSDGKYICAVTFPLGNAQSSTTVTLVBP-----TVSLIKGPDLSLDGGNET 188
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 HGLTVEDEGNYTCFATFPKSGVRGWTWLRVIAKPKQAQAKVTFSDQP-----T 178

Qy 189 VAAICIAATKPVVAHI-----DWEGLGEMESTTTTSPNETATIIISQYKLPTRFARGR 242
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG---TVTVTSRFTLVPSGRADGV 234

Qy 243 RITCVVHPALEKDIRYSFILDIOYAPESVSTGDNWFWGRKGNVLCNADANPPFPKS 302
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 TVTKVHESPEEPALIPVTLVSRYPPSVISGYDDNWLGRSEALTCDVRNPEPTGY 294

Qy 303 VWSRLDGQWPDGLASDNTLHFVHPLTFNYSVGVICKVNTSLGQSDQKVIYISDVPEKQ 362
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 DWSTTSPTPSAQAQSQL-VIHAVDSLFTTFTVCTVNAVGMGRABQVIFVRETP--N 351

Qy 363 TSSIAVAGAVIGAVLALFI-IAIFVTLLTPRKRPSYL-----DKVIDLPPTHKPP-P 414
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 TAGAGATGGIIGIIIAIATAVAATGLICRQQRKEQTLOGAEDEDELEGGPPSKPPTP 411

Qy 415 LYERSPPLPQK--DLQPEHLPIQTP-----KEREVGNLQHSNG----- 453
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 KAKLEAQEMPSQLFTLGASEHSPLKTPYFDAGASCTEQEMPRYHELPTLEERSGFLHPGA 471

Qy 454 -----LNSRSDYED-ENPVGEDGIQQWPLYNQMCVQDRSPGKHQNNND 497
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 TSLGSPDPVPPGPAVEDVSLDEDEGEHEEYLDKINPIYDALSYS--SPSDSYOG-- 527

Qy 498 PKRYVIDPREHY 510
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 528 --KGFVMSRAMYV 538

RESULT 5
HLMGP3
Poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A38211
R:Morrisson, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A:Reference number: A38211; MUID:92219365; PMID:1560525
A:Accession: A38211
A:Molecule type: DNA
A:Residues: 1-467 <MOR>
A:Cross-references: UNIPROT:P32507; GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:47-133/Domain: immunoglobulin homology <IMM1>
F:167-231/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM3>
F:355-374/Domain: transmembrane #status predicted <TMN>
F:375-467/Domain: intracellular #status predicted <INT>
F:54-131,174-229,274-320/Disulfide bonds: #status predicted
F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.3%; Score 467; DB 1; Length 467;
Best Local Similarity 32.5%; Pred. No. 1.2e-26;

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Matches 127; Conservative 57; Mismatches 171; Indels 36; Gaps 12;

Qy 30 LLOPPTPPPLLLPPLLLPRL- CGALAGPIIIEPHVHTAVWGNVSLKCLII---EYNETIT 87
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 VLPSPRLSPTLPLPLLLLLLLTGAQDVRVQVLPVGRGLGGTVELPCHLLPPTTERVS 65

Qy 88 QISWEKIHGKSSQTVAVHHPOYGSVOGEY--QGRVLP-----KNYSLNDATITLHNIG 139
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 QVTWQRLDG---TVAAAFHPSFGVDFPNSQFSKDRLSFVRARPETNADRLATLAFGLR 122

Qy 140 FSDGKYICAVTFPLGNAQSSTTVTLVBP-----TVSLIKGPDLSLDGGNETVAAICI 194
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 VEDEGNYTCFATFPNGTRGVTWLRVIAQENHAEAEVETIGQSV-----AVARCV 175

Qy 195 AATGKPVAHIDWEGDLGEMESTTTSPN---ETATIIISQYKLPTRFARGRRITCVVKHP 251
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 STGGRPPARITWISSLGG-EAKDTQEPGICQAGTIIISRYSLVPGVGRADGVKVTCTREHE 234

Qy 252 ALEKDIRYSFILDIOYAPESVSTGDNWFWGRKGNVLCNADANPPFPKSVWSRLDGQW 311
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 SFEPIILLPVTLSVRYPPSVISGYDDNWLGRSEALTCDVRNPEPTDYDMSTTSQVF 294

Qy 312 PDGLASDNTLHFVHPLTFNYSVGVICKVNTSLGQSDQKVIYISDVPEKQTS---SIATV 368
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 PASAVAQSQL-LVHSDVMWNTTICTATNAVGTGRAEQVILVTRDP--QASRDVGLV 351

Qy 369 AGAVIGAVLALFIAIFVT-VLLTPRKRPS 398
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 WGAVGTTLLVLLAGGLALILLRGRRRKS 382

RESULT 6
PRR2 alpha - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I53960
R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I53960
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-478 <RES>
A:Cross-references: UNIPROT:Q9UEI6; GB:S79171; NID:g1042202; PID:g1042203
C:Genetics:
A:Gene: PRR2alpha
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 16.8%; Score 455; DB 2; Length 478;
Best Local Similarity 30.3%; Pred. No. 9.5e-26;
Matches 121; Conservative 67; Mismatches 159; Indels 52; Gaps 13;

Qy 33 PPTPPPLLLPPLLLPRL- CGALAGPIIIEPHVHTAVWGNVSLKCLII---EYNETITQ 88
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 PPTP-----LLWPLLLLLLLTGAQDVRVQVLPVGRGLGGTVELPCHLLPPVGLYISL 67

Qy 89 ISWEKIHGKSS-QTVAVHHPOYGSVOGEYQ--RVLF-----KNYSLNDATITL 135
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 VTWRDPAPANHQAFAHFKMGSPFPSPKPGSRLSFVSAKQSTGQDTEAELQDATAL 127

Qy 136 HNIQFSDGKYICAVTFPLGNAQSSTTVTLVBP-----TVSLIKGPDLSLDGGNET 188
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 HGLTVEDEGNYTCFATFPKSGVRGWTWLRVIAKPKQAQAKVTFSDQP-----T 178

Qy 189 VAAICIAATKPVVAHI-----DWEGLGEMESTTTTSPNETATIIISQYKLPTRFARGR 242
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG---TVTVTSRFTLVPSGRADGV 234

Qy 243 RITCVVHPALEKDIRYSFILDIOYAPESVSTGDNWFWGRKGNVLCNADANPPFPKS 302
Dy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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A:Cross-references: GDB:I120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F:21-339/Domain: extracellular #status predicted <EXT>
F:21-339/Domain: extracellular #status predicted <EXT>
F:21-339/Domain: poliovirus receptor beta #status predicted <PVRB>
F:42-125/Domain: immunoglobulin homology <IMM1>
F:159-223/Domain: immunoglobulin homology <IMM2>
F:259-314/Domain: immunoglobulin homology <IMM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-417/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:I105,I20,188,I218,I237,I278,I307,I313/Binding site: carbohydrate (Asn) (covalent) #status pr:

Query Match 14.9%; Score 402; DB 1; Length 417;
Best Local Similarity 29.3%; Pred No. 6.3e-22;
Matches 106; Conservative 67; Mismatches 163; Indels 26; Gaps 11;

Qy 44 FPLLLFRSLCGAL-----AGPIIVE--PHVTAVMGKNVSLKCLIEVNET----ITQISWEK 93
Db 9 WFLLLVALLVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR 68
Qy 94 IHGKSSQTVAVHH---POYGRFSVQGEYQGRVLFKYNSLNDATITLHNIGFSDSGKYICKA 150
Db 69 -HGSSGSAVPHQTQGPSPYSKRLFEFAARL--GAELNANSLRMFLGRVDEDEGNYTCLF 125
Qy 151 VTFPLGNAQSSTTVTLVLEP--TVSLIIGPDSLIDGGNETVAALICAAATGKPVAHIDWEG 208
Db 126 VTFPGRSVDIWLKVLAKPONTAEVQKQLT-----GEVPWARCSTGGRPPAQITWHS 181
Qy 209 DLGSEMETT--TSPNETATTISQYKLPPTFEARGRRITCVVKKHPALEKDRIYSFLIDIQ 266
Db 182 DLGMPNTSQVPGFLSGITVTSLWILVPSQVDGKNVTKVEHESFEKPLLTVNLTVY 241
Qy 267 YAPSVTVTGYNWPFVGRKGNVKNKANADNPPPFKSVWSRLDGQWPDGLLASDNTLHFVH 326
Db 242 YPEVSIISGYDNNVYLGQNEATLTCDARSNPBPTGYNNWSTTMGTLPPFAVQAQAL-LIR 300
Qy 327 PLTFNYSGVYICKTNSIGORSQDKVVIYSIVPPFKTSSIAVAGAVIGALFLFIATFV 386
Db 301 PVDXPINTTLCNVTNALGARQAELTVQVKEGPPSEHSGMS-RNAIFLVILGILVFLILL 359
Qy 387 TV 388
Db 360 GI 361

RESULT 11
A54017
colon carcinoma-associated antigen pE4 precursor - rat
N:Alternate names: pE4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: A54017; A61206
R:Chadeneau, C.; LeMouillac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994.
A:Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinoma
A:Reference number: A54017; MUID:94253144; PMID:8195207
A:Accession: A54017
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <CHA>
A:Cross-references: UNIPROT:Q7M048; GB:I12025
R:Chadeneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.
Int. J. Cancer 47, 903-908, 1991
A:Title: Characterization, isolation and amino terminal sequencing of a rat colon carcinoma
A:Reference number: A61206; MUID:91184910; PMID:2010233
A:Accession: A61206
A:Molecule type: protein
A:Residues: 34-41, 'X', 43-53 <CH2>

Search completed: October 6, 2005, 10:21:11
Job time : 18.7671 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2005, 09:34:02 ; Search time 75.6517 Seconds
(without alignments)
3452.143 Million cell updates/sec

Title: US-09-972-268-12
Perfect score: 2707
Sequence: 1 MARTLRSPCLPGGKAQLS.....KHHQNDPKRYYIDPREHYV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.1*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 2388 | 88.2 | 510 | 2 Q9JLB8 | Q9JLB8 mus musculus |
| 2 | 2107 | 77.8 | 438 | 2 Q9JLB7 | Q9JLB7 mus musculus |
| 3 | 1920.5 | 70.9 | 549 | 2 Q9NQ53 | Q9NQ53 homo sapien |
| 4 | 1872 | 69.2 | 366 | 2 Q6NV23 | Q6NV23 homo sapien |
| 5 | 1819.5 | 67.2 | 549 | 2 Q9JLB9 | Q9JLB9 mus musculus |
| 6 | 1775.5 | 65.6 | 549 | 2 Q9JLB6 | Q9JLB6 mus musculus |
| 7 | 1235 | 45.6 | 267 | 2 Q8NC05 | Q8NC05 homo sapien |
| 8 | 1173.5 | 43.4 | 407 | 2 Q9Y412 | Q9Y412 homo sapien |
| 9 | 648.5 | 24.0 | 304 | 2 Q9BVA9 | Q9BVA9 homo sapien |
| 10 | 602 | 22.2 | 515 | 1 PVR1 MOUSE | Q9Jkf6 mus musculus |
| 11 | 598 | 22.1 | 515 | 2 Q6P9F9 | Q6P9m9 mus musculus |
| 12 | 589 | 21.8 | 515 | 1 PVR1_FIG | Q9gl76 sus scrofa |
| 13 | 588 | 21.7 | 517 | 1 PVR1 HUMAN | Q15223 homo sapien |
| 14 | 540 | 19.9 | 530 | 1 PVR2 MOUSE | P32507 mus musculus |
| 15 | 537 | 19.8 | 530 | 2 Q8QX35 | Q8QXJ5 mus musculus |
| 16 | 534.5 | 19.7 | 295 | 2 Q9ERF5 | Q9erf5 mesocricetu |
| 17 | 528 | 19.5 | 298 | 2 Q9GL74 | Q9gl74 cercopithec |
| 18 | 527 | 19.5 | 538 | 1 PVR2 HUMAN | Q92692 homo sapien |
| 19 | 526.5 | 19.4 | 295 | 2 Q9GL75 | Q9gl75 bos taurus |
| 20 | 523.5 | 19.3 | 510 | 2 Q96N78 | Q96ny8 homo sapien |
| 21 | 522.5 | 19.3 | 510 | 2 Q96K15 | Q96kl5 homo sapien |
| 22 | 511.5 | 18.9 | 483 | 2 Q9DBP8 | Q9dbp8 mus musculus |
| 23 | 503.5 | 18.6 | 464 | 2 Q9GL25 | Q9gl25 xenopus tro |
| 24 | 495 | 18.3 | 508 | 2 Q8CED8 | Q8ced8 mus musculus |
| 25 | 495 | 18.3 | 508 | 2 Q8R007 | Q8r007 mus musculus |
| 26 | 494 | 18.2 | 463 | 2 Q66J72 | Q66j72 xenopus lae |
| 27 | 467 | 17.3 | 467 | 2 Q8C6F2 | Q8c6f2 mus musculus |
| 28 | 467 | 17.3 | 467 | 2 Q91VT9 | Q91vt9 mus musculus |
| 29 | 427.5 | 15.8 | 449 | 2 Q9UE16 | Q9ue16 homo sapien |
| 30 | 418 | 15.4 | 417 | 1 PVR_CERAE | P32506 cercopithec |
| 31 | 411.5 | 15.2 | 412 | 2 Q9R1E1 | Q9r1e1 rattus norv |

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32 407 15.0 400 2 Q8HY16      Q8hy16 cebus apell
33 406.5 15.0 412 2 Q63611    Q63611 rattus norv
34 405 15.0 417 1 PVR_HUMAN  P15151 homo sapien
35 402.5 14.9 408 2 Q91WP1    Q91wp1 mus musculus
36 400.5 14.8 408 2 Q8K094    Q8k094 m hypotheri
37 399.5 14.8 408 2 Q8BVF6    Q8bvf6 mus musculus
38 395 14.6 401 2 Q88835    Q88835 cercopithec
39 390 14.4 403 2 Q8HY15    Q8hy15 lemur catta
40 386 14.3 412 2 Q8HY14    Q8hy14 oryctolegus
41 355.5 13.1 415 2 Q60977    Q60977 mus musculus
42 326.5 12.1 416 2 Q7M048    Q7m048 rattus norv
43 309 11.4 417 2 Q7TNL1    Q7tnl1 mus musculus
44 305.5 11.3 442 2 Q9BY67    Q9by67 homo sapien
45 304.5 11.2 390 2 Q66KX2    Q66kx2 xenopus lae

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ALIGNMENTS

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RESULT 1
Q9JLB8 PRELIMINARY; PRT; 510 AA.
AC Q9JLB8;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 beta.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195834; AAF63686.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 510 AA; 55811 MW; 45CF6EF78454864 CRC64;

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Query Match 88.2%; Score 2388; DB 2; Length 510;
Best Local Similarity 88.8%; Pred. No. 1.7e-171;
Matches 454; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

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Qy 1 MARTLRSPCLPGGKAQLSSASLLGALLLOPPPPPLLLLLPPLILFSLRCALAGPI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARTPGPAPLCPGGKAQLSSAFPPAAGLLLPATPPPLLLLLLPPLILFSLRCALAGSI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 IVPEPHTVAVGKGVSKLIEVNETIQTISWEKIHGKSSQTVAVHHPOYGFVSOGYQGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IVPEPHTVAVGKGVSKLIEVNETIQTISWEKIHGKSTQTVAVHHPOYGFVSOGYQGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPD 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 181 LIDGNGTVAACIAATGKPVAHIDWEGDLGEMSTTSPNETATIIISQKLPPTFAR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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| | | | |
|--|--|---|-----|
| Db | 181 | LIDGGNETVAACVAAATGKPAQIDWEGDLGEMESSTTSPNETATIVSQYKLPFTRFAR | 240 |
| Qy | 241 | GRITCVKHPALEKDIRSFILDIQYAPEVSVTGDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Db | 241 | GRITCVKHPALEKDIRSFILDIQYAPEVSVTGDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Qy | 301 | KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYCKVTNSLGORSQDKVIYISDVPF | 360 |
| Db | 301 | KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYCKVTNSLGORSQDKVIYISDVPL | 360 |
| Qy | 361 | KOTSSIAVAGAVIGAVLALFIIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS | 420 |
| Db | 361 | TQTSSIAVAGAVIGAVLALFIIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPVYEERI | 420 |
| Qy | 421 | PPLPQKDLF-QPHLPLQTFQKREVRGNLOHNSGRSFDYEDENPVGSDGTQOMVPLY | 479 |
| Db | 421 | PSLPQKDLGQTEHLPLQTFQKKGAGLQSPNGPISRRFDYEDESTMQEDGTQRMCPLY | 480 |
| Qy | 480 | NOMCYODRSPGKHQNDPKRVVIDPREHYV | 510 |
| Db | 481 | SQMCHQDRSPRQHPRN-PERLYINPREHYV | 510 |
| RESULT 2 | | | |
| Q9JLB7 | ID | Q9JLB7 PRELIMINARY; PRT; 438 AA. | |
| AC | Q9JLB7 | | |
| DT | 01-OCT-2000 (TReMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TReMBLrel. 15, Last sequence update) | | |
| DT | 01-MAR-2004 (TReMBLrel. 26, Last annotation update) | | |
| DE | Cell adhesion molecule nectin-3 gamma. | | |
| GN | Name=Pvr13; | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291; | | |
| RA | Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M., | | |
| RA | Tachibana K., Mizoguchi A., Takai Y.; | | |
| RT | "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules | | |
| RT | that shows homophilic and heterophilic cell-cell adhesion | | |
| RT | activities."; | | |
| RL | J. Biol. Chem. 275:10291-10299 (2000). | | |
| DR | EMBL; AF195835; AAF63687.1; -. | | |
| DR | MGI; 1930171; Pvr13. | | |
| DR | GO; GO:0005913; C:cell-cell adherens junction; IDA. | | |
| DR | GO; GO:0005615; C:extracellular space; TAS. | | |
| DR | GO; GO:0016021; C:integral to membrane; TAS. | | |
| DR | GO; GO:0005515; F:protein binding; IPI. | | |
| DR | GO; GO:0016337; P:cell-cell adhesion; IDA. | | |
| DR | InterPro; IPR003599; Ig. | | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | Pfam; PF00047; Ig; 1. | | |
| DR | SMART; SM00409; IG_LIKE; 3. | | |
| DR | PROSITE; PS00835; IG_LIKE; 3. | | |
| SQ | SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64; | | |
| Query Match 77.8%; Score 2107; DB 2; Length 438; | | | |
| Best Local Similarity 93.2%; Pred. No. 2.1e-150; | | | |
| Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0; | | | |
| Qy | 1 | MARTLRPSLPCGGGKAQLSSALLGAGLLQLQPTPPPLLLLFPLLLFSRLCGALAGPI | 60 |
| Db | 1 | MARTPGAPLPCGGGKAQLSSAPPAAGLLLPAPTPPPPLLLLIPLLLFSRLCGALAGSI | 60 |
| Qy | 61 | IVEPHVTVAVGKGVNLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFVSQVQYQGR | 120 |
| Db | 61 | IVEPHVTVAVGKGVNLKCLIEVNETITQISWEKHGKSTQTVAVHHPQYGFVSQVQYQGR | 120 |
| Qy | 121 | VLFNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVVEPTVSLIKGPD | 180 |
| Query Match 70.9%; Score 1920.5; DB 2; Length 549; | | | |
| Best Local Similarity 67.9%; Pred. No. 3.4e-136; | | | |
| Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10; | | | |
| Qy | 1 | MARTLRPSLPCGGGKAQLSSALLGAGLLQLQPTPPPLLLLFPLLLFSRLCGALAGPI | 60 |
| Db | 1 | MARTLRPSLPCGGGKAQLSSALLGAGLLQLQPTPPPLLLLFPLLLFSRLCGALAGPI | 60 |
| Qy | 61 | IVEPHVTVAVGKGVNLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFVSQVQYQGR | 120 |
| Db | 61 | IVEPHVTVAVGKGVNLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFVSQVQYQGR | 120 |
| Qy | 121 | VLFNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVVEPTVSLIKGPD | 180 |
| Db | 121 | VLFNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVVEPTVSLIKGPD | 180 |
| Qy | 181 | LIDGGNETVAAICIAATGKPAQIDWEGDLGEMESSTTSPNETATIIISOYKLPFTRFAR | 240 |
| Db | 181 | LIDGGNETVAAICIAATGKPAQIDWEGDLGEMESSTTSPNETATIIISOYKLPFTRFAR | 240 |
| Qy | 241 | GRITCVKHPALEKDIRSFILDIQYAPEVSVTGDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Db | 241 | GRITCVKHPALEKDIRSFILDIQYAPEVSVTGDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Qy | 301 | KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYCKVTNSLGORSQDKVIYISDVPF | 360 |
| Db | 301 | KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYCKVTNSLGORSQDKVIYISDVPL | 360 |
| Qy | 361 | KOTSSIAVAGAVIGAVLALFIIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS | 420 |
| Db | 361 | TQTSSIAVAGAVIGAVLALFIIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPVYEERI | 420 |
| Qy | 421 | PPLPQKDL 428 | |
| Db | 421 | PSLPQKDL 428 | |
| RESULT 3 | | | |
| Q9NQS3 | ID | Q9NQS3 PRELIMINARY; PRT; 549 AA. | |
| AC | Q9NQS3 | | |
| DT | 01-OCT-2000 (TReMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TReMBLrel. 15, Last sequence update) | | |
| DT | 01-OCT-2003 (TReMBLrel. 25, Last annotation update) | | |
| DE | Nectin 3. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G., | | |
| RA | Dubreuil P., Lopez M.; | | |
| RT | "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that | | |
| RT | interacts with afadin."; | | |
| RL | Gene 0:0-0(2000). | | |
| DR | EMBL; AF282874; AAF97597.1; -. | | |
| DR | InterPro; IPR003599; Ig. | | |
| DR | InterPro; IPR007110; Ig-like. | | |
| DR | Pfam; PF00047; Ig; 1. | | |
| DR | SMART; SM00409; IG_LIKE; 3. | | |
| DR | PROSITE; PS00835; IG_LIKE; 3. | | |
| SQ | SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64; | | |

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Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVISDP- 359
Db 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVISDPPT 360
Qy 360 -----FKQTSIAVAGAVIGALVALFIIA 383
Db 361 TTTTLOPTQIOWHPSTADIEDLATEPKLPPLPPLSTLATIKDDTIIAIIASVVGALFIVLS 420
Qy 384 IFVTVLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424
Db 421 VLAGIFCYRRRTTRGDFYAKNY-IPPSDMQKESQIDVLQODELSDYPSVKKENKPV- 478
Qy 425 QKDLFQPEHL--PLOTQKEREVENLOHNSGNSRSPYEDENPVGSDGTOOMPLYNQM 482
Db 479 -NNLIRKDYLEBPEKTQW-----NNVENLNRF-ERPMDYEDLQKGMKRFVSD----- 523
Qy 483 CYQDRSPGKHQNNPKRV-----YTDPRHYV 510
Db 524 -----EHYDENEDDLVSHVDGVSISRREWYV 549

RESULT 4
Q6NVZ3 PRELIMINARY; PRT; 366 AA.
AC Q6NVZ3, 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE VRL3 protein.
GN Name=VRL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Stalska U., Smallos D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067808; AAH67808.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 366 AA; 39722 MW; 591D0A4697C30BA CRC64;
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Query Match

69.2%; Score 1872; DB 2; Length 366;

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Best Local Similarity 99.7%; Pred. No. 8.9e-133;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MARTLRSPICPGGKAQLSSASLLGALLQPPPTPPPLLLFRLCGALAGPI 60
Db 1 MARTLRSPICPGGKAQLSSASLLGALLQPPPTPPPLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFSGVQYQGR 120
Qy 121 VLFQNSLNDATTTLNIGFSDSGKYICKAVTTPPLGNAQSTTTVTLVEPTVSLIKGPD 180
Db 121 VLFQNSLNDATTTLNIGFSDSGKYICKAVTTPPLGNAQSTTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATTISQYKLPPTPAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATTISQYKLPPTPAR 240
Qy 241 GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGNLKNADANPPF 300
Db 241 GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGNLKNADANPPF 300
Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVIS 356
Db 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIIVIS 356

RESULT 5
Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9, 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Cell adhesion molecule nectin-3 alpha.
GN Name=Pvrl3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20299403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities."
RL J. Biol. Chem. 275:10291-10299 (2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60582 MW; 5492C9ABB472F185 CRC64;
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Query Match

67.2%; Score 1819.5; DB 2; Length 549;

Best Local Similarity 68.2%; Pred. No. 1.4e-128; Matches 369; Conservative 35; Mismatches 60; Indels 77; Gaps 9;

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Qy 1 MARTLRSPICPGGKAQLSSASLLGALLQPPPTPPPLLLFRLCGALAGPI 60
Db 1 MARTLRSPICPGGKAQLSSASLLGALLQPPPTPPPLLLFRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKHGSSQTVAVHHPOYGFSGVQYQGR 120
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Qy 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPP 300
Db 241 GRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPP 300
Qy 301 KSVWSRLDQWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVPF 360
Db 301 KSVWSRLDQWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVPF 360
Qy 361 KQT-----SSIA-----VAGAVIGAVIALFIIA 383
Db 361 TTTLQPTVQWHSSPADVDIATEHKLPPLSTLTKDDTTIGTIIASVVGALFLVLVS 420
Qy 384 IFVTVLTPRKR-----PSYLDKVIDLPPHK-----PPPLYEERSPLPQ 425
Db 421 ILAGVFCYRRRTFRGDFYAKNYIPPSDMQKESQIDVLHODELSDYPSVCKENKNP-- 478
Qy 426 KDLFQPEHL--PLOTQFKEREVGLQHSNGLNSRSDYDENPNVG-----EDG 471
Db 479 NNLIRKDYLEBEPTQW--NNVENLTRF----ERPMDYEDLKMGMKFSVDERVNESEDG 532
Qy 472 I 472
Db 533 L 533

RESULT 7
Q8NC05
ID Q8NC05 PRELIMINARY; PRT; 267 AA.
AC Q8NC05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Negahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 267 AA; 29253 MW; 4F4648A81BA0C451 CRC64;

Query Match 45.6%; Score 1235; DB 2; Length 267;
Best Local Similarity 96.0%; Pred. No. 6.5e-85;
Matches 242; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 41 LLLPPLL--LPSRLCGALAGPIIVEPHVTAWGNVSLKCLIEVNETITQISWEKINGKS 98
Db 16 LLRGPLLPSFGSNPRALAGPIIVEPHVTAWGNVSLKCLIEVNETITQISWEKINGKS 75
Qy 99 SQTVAVHHPOYGFSGVQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNA 158
Db 76 SQTVAVHHPOYGFSGVQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNA 135
Qy 159 QSSTTVTVLVEPTVSLKIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 218
Db 136 QSSTTVTVLVEPTVSLKIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 195
Qy 219 SFPNETATISQYKLPFTRFARGRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYD 278
Db 219 SFPNETATISQYKLPFTRFARGRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYD 278
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Db 196 SFPNETATISQYKLPFTRFARGRRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYD 255
Qy 279 NWFVGRKGVNLK 290
Db 256 NWFVGRKGVNLK 267

RESULT 8
Q9Y412
ID Q9Y412 PRELIMINARY; PRT; 407 AA.
AC Q9Y412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp566B0846 (fragment).
GN Name=DKFZp566B0846;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Oosterwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -
DR PIR; T08732; T08732.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 43.4%; Score 1173.5; DB 2; Length 407;
Best Local Similarity 62.8%; Pred. No. 5e-80;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Qy 143 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLKIDGGNETVAAICIAATGK 202
Db 1 SGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLKIDGGNETVAAICIAATGK 60
Qy 203 HIWEGDLGEMESTTSPNETATISQYKLPFTRFARGRRITCVVHPALEKDIRYSFI 262
Db 61 HIWEGDLGEMESTTSPNETATISQYKLPFTRFARGRRITCVVHPALEKDIRYSFI 120
Qy 263 LDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPKSVWSRLDQWPDLGLASDNTL 322
Db 121 LDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPKSVWSRLDQWPDLGLASDNTL 180
Qy 323 HFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP----- 359
Db 181 HFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP----- 240
Qy 360 -----FKQTSSIAVAGAVIGAVIALFIIAFTVLLTPRKK--RSYLDKV 403
Db 241 EPKKLPPLSTLATIKDDTTIIASVVGALFVLVSILAGIFCYRRRTFRGDFYAKN 300
Qy 404 IDLPPTH-----KPPPLYEERSPLPQKDLFOPEHL--PLOTQFKEREV 446
Db 301 Y-IPPSDMQKESQIDVLQDELDPYPSVCKENKNVNNLIRKDYLEBEPTQW-----N 354
Qy 447 NLQHSNGLNSRSDYDENPNVG 468
Db 355 NVENLNRF-ERPMDYEDLQMG 375

RESULT 9
Q9BVA9
ID Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```


Db 44 GTDVLVHCSFANPLPSVKITQVTWQKASNGSKONMAIYNPTMGVSVLPPEYKRVFELRPS 103
Qy 128 LNDATITLHNTGSDSGKIYKAVTFPLGNAQSSTVTVLVEPTVSLIKGSDSLDG--- 184
Db 104 FIDGTIRLSGLEDEGMYICEFATFPGNRESQNLNVTMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAICAATGKPVAHIDWEGDL-GEMESTTSPNETATIIISOYKLPFTRFARGR 242
Db 163 QDNKVLVATCANGKPPSAVSWETRLKGEAYQIRPNPNTVTVISRYLRVPSREAHQ 222
Qy 243 RITCVKHPALEKDIRYFILDIOYAPESVTVGDNMFVGRKGVNLCNADANPPPPPKS 302
Db 223 SLACIVNY-HLDR-FRESLTANVOYEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEY 280
Qy 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQSDQKVIYISDVPPKQ 362
Db 281 HWTTLNGLPKGVEAQNRTLFFRGPIYSLAGTYICEATNPITGRSGQGVENITEFPYTP 340
Qy 363 TSS-----IAVAGAVIGAVLAFIIFVTVLLTPRKKPSYLDKVIDLPTHKPP 413
Db 341 TPEHRRAGQMPATAIIGVAGSVLLVIVGGIIVAL-RRRRHTF----- 384
Qy 414 PLYEERSPPLPKOLFQ-----PEHLPLQTPKEREVGNLQK-----SNGLSN 456
Db 395 -----KGDYSTKXHYNGYSGKAGIPQHPPMAQ-----NLQYPPDSDDEKKASPLGG 432
Qy 457 RSFYEDENPVGEDGIQOM-----YPLYN-----QMCYQDRSPGKHQND 497
Db 433 SSYBEEEGGGGGERKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRTLGYQY---D 489
Qy 498 PKRV-----YIDPREHYV 510
Db 490 PEQLDAENMVSNQDGSFISKKEWYV 515

RESULT 11

Q6P9M9 PRELIMINARY; PRT; 515 AA.
ID Q6P9M9
AC Q6P9M9
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Poliovirus receptor-related 1.
GN Name=Pvrl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060694; AAH60694.1; -
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;
Query Match 22.1%; Score 598; DB 2; Length 515;
Best Local Similarity 31.0%; Pred. No. 1.8e-36;
Matches 155; Conservative 86; Mismatches 171; Indels 88; Gaps 16;
Qy 71 GKNVSLKCLIE--VNETITQISWEKIHGKSSQTVAVHHPOYGFSGVEYQGRVLFRNYS 127
Db 44 GTDVLVHCSFANPLPSVKITQVTWQKASNGSKONMAIYNPTMGVSVLPPEYKRVFELRPS 103
Qy 128 LNDATITLHNTGSDSGKIYKAVTFPLGNAQSSTVTVLVEPTVSLIKGSDSLDG--- 184
Db 104 FIDGTIRLSGLEDEGMYICEFATFPGNRESQNLNVTMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAICAATGKPVAHIDWEGDL-GEMESTTSPNETATIIISOYKLPFTRFARGR 242
Db 163 QDDKVLVATCANGKPPSAVSWETRLKGEAYQIRPNPNTVTVISRYLRVPSREAHQ 222
Qy 243 RITCVKHPALEKDIRYFILDIOYAPESVTVGDNMFVGRKGVNLCNADANPPPPPKS 302
Db 223 SLACIVNY-HLDR-FRESLTANVOYEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEY 280
Qy 303 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQSDQKVIYISDVPPKQ 362
Db 281 HWTTLNGLPKGVEAQNRTLFFRGPIYSLAGTYICEATNPITGRSGQGVENITEFPYTP 340
Qy 363 TSS-----IAVAGAVIGAVLAFIIFVTVLLTPRKK--RPSYLDK----- 402
Db 341 TPEHRRAGQMPATAIIGVAGSVLLVIVGGIIVALRRRHTPKGDYSTKXHYNGYSG 400
Qy 403 VIDLPFTHKPPPLYEERSPPLPKOLFQPEHLPLQTPKEREVGNLQHSNGLNSRSPDYE 462
Db 401 KAGIPQHH--PPMAQNLQYPPDSD-----EKKAGPLGGS-----SYEE 438
Qy 463 DENPVGEDGTQOM---YPLYN-----QMCYQDRSPGKHQNDPKRV-- 501
Db 439 EEEEGGGGGERKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRTLGYQY---DPEQLDL 495
Qy 502 -----YIDPREHYV 510
Db 496 AENMVSNQDGSFISKKEWYV 515
RESULT 12
ID PVRL1_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1).
GN Name=PVRL1; Synonyms=HVEC, PRR1;

OS Sus scrofa (Pig).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
 RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
 RA Cohen G.H.;
 RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
 RT is a functional alphaherpesvirus receptor.";
 RL Virology 281:315-328(2001).
 CC -1- FUNCTION: Probably involved in cell adhesion. Receptor for
 CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
 CC cells.
 CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gp) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF308632; AAC30281.1; -;
 DR HSPG; Q05793; 1GL4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 30
 FT CHAIN 31 515
 FT DOMAIN 31 355
 FT TRANSMEM 356 376
 FT DOMAIN 377 515
 FT DOMAIN 31 141
 FT DOMAIN 145 243
 FT DOMAIN 247 334
 FT DOMAIN 437 443
 FT DOMAIN 444 447
 FT DISULFID 51 124
 FT DISULFID 172 226
 FT DISULFID 269 316
 FT CARBOHYD 36 36
 FT CARBOHYD 72 72
 FT CARBOHYD 139 139
 FT CARBOHYD 202 202
 FT CARBOHYD 286 286
 FT CARBOHYD 297 297
 FT CARBOHYD 307 307
 FT CARBOHYD 332 332
 SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;
 Query Match 21.8%; Score 589; DB 1; Length 515;
 Best Local Similarity 30.2%; Pred. No. 8.4e-36;
 Matches 156; Conservative 83; Mismatches 194; Indels 84; Gaps 15;
 QY 52 LCGALAGPIIPEPHVTAWGKNSVSKLIE---VNETITQISWEKIHGKSSQTVAVHPQ 108
 DB 25 LPGAHTQVQVNDMSYGFIDGTVLHCSFANPLPGVKITQVTWQKATGSKQNVAIYNP 84
 QY 109 YGFSVQGEYQGRVLKPKVSLNDATITLHNIGFSGSKYICKAVTFPLGNQSSSTTVLV 168
 DB 85 MGVSLAPYRERVRFLRPSFTDGTIRLSRLEDEGVYICFEPATFPAGNRSLNLTVA 144
 QY 169 EPTVSLIKGPDSLIDG---GNETVAICIAATKPKVAHIDWEGDL-GEMESTTTSFPNE 223

Db 145 KPT-NWIEGTQAVLRAKKGDKDLVATCTSANGKPPSVVSWETHLKGEAEYQEIERNPG 203
 QY 224 TATIISOYKLFTRFARGRRITCVVKHPALEKDIRYSFILDIOYAEVSVGTGDNWFGV 283
 Db 204 TVTVISRYRLVPSREDHROSCLACIVNYHM--DRFRESLTINVQYEPEVTIEGDFGNWY 261
 QY 284 RKGVLNLCNADANPPPFKSVWSRLDGOWPDGILLASDNTLHFVHPLTFNYSGVVICKVTNS 343
 Db 262 RMDVKLTCKADANPPATEYHWTTLNGLSLPKGVEAQNRTLFFRGPIYNSMAGTICATNP 321
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 Db 322 IGRSQVEVNIETFPYTPSPPEHGRRAQOVPTAIIIGVVVGSILLVLFVVGGIIVALCRR 381
 QY 393 RKK-RPSYLDK-----VIDLPPTHKPPPYEERSPPLPKQKOLFQEPHLPLOTFKE 442
 Db 382 RHTFKGDYTKKHVYNGYSGKAGIPQHH--PPMAQNLOYPEDSD-----E 425
 QY 443 REVGNLQHSNLSRSDYEDENPVGEGDIGQMYPLYN-----OMCYQD 486
 Db 426 KKAGPL-----GSSYEEEEEGERKVGPHPKYDEDAKRPYTVDEAEARQDGYGD 481
 QY 487 RSPGKHQNNDKRV-----YIDPREHYV 510
 Db 482 RTLGYQY---DPEQLDLAENMVYSDNGSFISKKEWIV 515
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 ID PVRI_HUMAN Q15223; O75465; Q9HBE6; Q9HBW2;
 AC Q15223; O75465; Q9HBE6; Q9HBW2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
 DE mediator C) (HveC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
 DE (CD111 antigen).
 GN Names=PVRI1; Synonyms=HVEC, PRR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G;
 RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
 RA Dubreuil P.;
 RT "cDNA characterization and chromosomal localization of a gene related
 RT to the poliovirus receptor gene.";
 RL Gene 155:261-265(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=98279152; PubMed=9616127; DOI=10.1126/science.280.5369.1618;
 RA Garaghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
 RA Spear P.G.;
 RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
 RT protein 1 and poliovirus receptor.";
 RL Science 280:1618-1620(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=21256041; PubMed=11356977;
 RX DOI=10.1128/JVI.75.12.5684-5691.2001;
 RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
 RA Campadelli-Fiume G., Dubreuil P.;
 RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
 RT nectin1 (or pr1-HIGR-Hvec) modulates positively and negatively
 RT susceptibility to hsv infection.";
 RL J. Virol. 75:5684-5691(2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
 RX MEDLINE=20392396; PubMed=10932188; DOI=10.1038/78119;
 RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,


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RESULT 14
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ID PVR2_MOUSE STANDARD; PRT; 530 AA.
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
entry protein B) (HvEB) (Nectin 2) (Poliovirus receptor homolog).
GN Name=Pvr12; Synonyms=Mph, Pvr, Pvs;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RP MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
poliovirus receptor gene.";
RL J. Virol. 66:2807-2813 (1992).
RN [2]
SEQUENCE FROM N.A. (ISOFORM BETA).
RP STRAIN=C57BL/6; TISSUE=Brain;
RX STRAIN=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
interaction with poliovirus.";
RL J. Biol. Chem. 269:8431-8438 (1994).
RN [3]
SEQUENCE FROM N.A. (ISOFORM BETA).
RP STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Umedin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Bailey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnur A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
CHARACTERIZATION.
RP MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)
mediates entry of pseudorabies virus but not herpes simplex virus
types 1 and 2.";
RL J. Virol. 73:4493-4497 (1999).
CC -!- FUNCTION: Receptor for alphaherpesvirus (such as murine HSV) entry
into cells.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
liver.

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CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; M80206; AAA39734.1; -.
CC EMBL; D26107; BAA05103.1; -.
CC EMBL; BC059941; AAH59941.1; -.
CC PIR; A38211; HLMSP3.
CC PIR; A53437; A53437.
CC MGD; MGI:97822; Pvr12.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig; 3.
CC PROSITE; PS50835; IG_LIKE; 3.
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KW Repeat; Signal; Transmembrane.
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FT CHAIN 32 530 Poliovirus receptor related protein 2.
FT DOMAIN 32 351 Extracellular (Potential).
FT TRANSMEM 352 372 Potential.
FT DOMAIN 373 530 Cytoplasmic (Potential).
FT DOMAIN 32 147 Ig-like V-type.
FT DOMAIN 153 247 Ig-like C2-type 1.
FT DOMAIN 252 337 Ig-like C2-type 2.
FT DISULFID 54 131 By similarity.
FT DISULFID 174 229 By similarity.
FT DISULFID 274 320 By similarity.
FT CARBOHYD 128 138 N-linked (GlcNAc...) (Potential).
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FT Missing (in isoform Alpha).
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QY 88 QISWEKIHGKSSQTVAHHPOYGFSGVEY--QGRVLF-----KNYSINDATITLHNIG 139
DB 66 QVTWQRLDG---TVVAFAHFSGVDFPNQSFSDRLSFVRARPETNADLRDIAFLRGLR 122
QY 140 FSDSGKYICKAVTFPLGNAQSSTVTVLVLP-----TVSLIKGPDSLIDGNETVAIIC 194
DB 123 VEDEGNYTCFATFPNGTRGVTLRVIAQENHAEQVETIGPQSV-----AVARCV 175
QY 195 AATGKPVAHIDWEGDLGEMESTTSPFN---ETATITISQYKLPPTFRFARGRITCVVGH 251
DB 176 STGGRPPARITWISSLGG-EAKDTQSPGIQAGVTIISRYSLVFPVGRADGVKVTCTREHE 234
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 21.3581 Seconds
(without alignments)
1782.508 Million cell updates/sec

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Perfect score: 2707

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 588 | 21.7 | 517 | US-09-723-368-4 | Sequence 4, Appli |
| 3 | 584.5 | 21.6 | 458 | US-09-435-956A-1 | Sequence 1, Appli |
| 4 | 565.5 | 20.9 | 518 | US-09-919-172-20 | Sequence 20, Appl |
| 5 | 465 | 17.2 | 522 | US-09-949-016-7563 | Sequence 7563, Ap |
| 6 | 458.5 | 16.9 | 479 | US-09-723-368-2 | Sequence 2, Appli |
| 7 | 458.5 | 16.9 | 479 | US-09-949-016-6278 | Sequence 6278, Ap |
| 8 | 406 | 15.0 | 456 | US-09-949-016-7564 | Sequence 7564, Ap |
| 9 | 402 | 14.9 | 417 | US-09-949-016-6729 | Sequence 6729, Ap |
| 10 | 400.5 | 14.8 | 408 | US-09-724-864-62 | Sequence 62, Appl |
| 11 | 306.5 | 11.3 | 442 | US-09-778-510-20 | Sequence 20, Appl |
| 12 | 306.5 | 11.3 | 442 | US-09-930-803-1 | Sequence 1, Appli |
| 13 | 304.5 | 11.2 | 440 | US-09-866-028-61 | Sequence 61, Appl |
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| 15 | 290.5 | 10.7 | 423 | US-09-778-510-22 | Sequence 22, Appl |
| 16 | 285.5 | 9.4 | 398 | US-09-778-510-4 | Sequence 4, Appli |
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| 18 | 248.5 | 9.2 | 398 | US-09-907-794A-84 | Sequence 84, Appl |
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33 199 7.4 1101 3 US-08-986-485-2 Sequence 2, Appli
34 190.5 7.0 227 4 US-09-205-258-947 Sequence 947, App
35 187.5 6.9 274 3 US-09-570-367C-19 Sequence 19, Appl
36 187.5 6.9 274 4 US-09-915-524-19 Sequence 19, Appl
37 187.5 6.9 274 4 US-09-934-634-19 Sequence 19, Appl
38 178.5 6.6 467 3 US-09-046-736-2 Sequence 2, Appli
39 177 6.5 626 4 US-09-949-016-6213 Sequence 6213, Ap
40 177 6.5 664 4 US-09-949-016-7850 Sequence 7850, Ap
41 175 6.5 387 3 US-09-175-928-2 Sequence 2, Appli
42 175 6.5 819 4 US-09-949-016-11044 Sequence 11044, A
43 175 6.5 837 4 US-09-949-016-6515 Sequence 6515, Ap
44 174 6.4 511 4 US-09-949-016-10054 Sequence 10054, A
45 174 6.4 1091 3 US-08-986-485-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-11380
; Sequence 11380, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11380
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11380

Query Match 21.7%; Score 588; DB 4; Length 514;
Best Local Similarity 30.1%; Pred. No. 1.2e-46;
Matches 151; Conservative 85; Mismatches 176; Indels 90; Gaps 15;
Qy 71 GKNVSLKLIB---VNETITQISWEKTHGKSSQTVAVHHPQYGFSGVOQYGRVLFKNYS 127
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Qy 502 -----YIDPREHYV 510
Db 493 DLAENMVSONDGSFISKKEWV 514
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RESULT 2

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US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/201
; CURRENT APPLICATION NUMBER: US/09/723.368
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: U.S. 60/087.862
; PRIOR FILING DATE: 1998-06-03
; PRIOR FILING DATE: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4
```

```
Query Match 21.7%; Score 588; DB 4; Length 517;
Best Local Similarity 30.1%; Pred. No. 1.2e-46;
Matches 151; Conservative 85; Mismatches 176; Indels 90; Gaps 15;

Qy 71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKONVAIYNPSMGVSLAPYRVERVEFLRPS 103

Qy 128 LNDATITLHNI GFSDSGKYCKAVTPPLGNAQSTTTVTLVPEVTSLIKGPDSLIG--- 184
Db 104 FTDGTIRLSRLEDEGVYICEFATPTGNRESQLNTVMAKPT-NWIEGTQAVLRAKKG 162

Qy 185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTSPNETATIIISOYKLFPTFRAGR 242
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAYQIEIRNPNGTIVTISRVLVPSREAHQ 222

Qy 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGNLKNADANPPPFKS 302
Db 223 SLACIVNYHM--DRFKESLTUNVQYEVETIEGFGNWLQRMVDKLTCKADANPPATEY 280

Qy 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGORSQDKVIYISDVFPKQ 362
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPICTRSGQVEVNITEKPYTP 340

Qy 363 TS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDK----- 402
```

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Db 341 SPPEHRRAGPVPTAIIIGVAGSILLVIVGGIVVALRRRHTFKGDYSTKKHVGNGY 400
Qy 403 -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSDY 461
Db 401 SKAGIPQHH--PPMAQNLOYPDDSD--EKKAGPLGGS-----SYEE 438
Qy 462 EDENPVGEDGIQOM---YPLYN-----QMCYQDRSPGKHQNNDPKRV 501
Db 439 EEEEEGGGGERKVGPHKPYDDEAKRPYFTVDEAEARQDGYGDRTLGYQY---DPEQL 495
Qy 502 -----YIDPREHYV 510
Db 496 DLAENMVSONDGSFISKKEWV 517
```

RESULT 3

```
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435.956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1
```

```
Query Match 21.6%; Score 584.5; DB 4; Length 458;
Best Local Similarity 35.5%; Pred. No. 2.1e-46;
Matches 137; Conservative 67; Mismatches 165; Indels 17; Gaps 9;

Qy 71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGSVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKONVAIYNPSMGVSLAPYRVERVEFLRPS 103

Qy 128 LNDATITLHNI GFSDSGKYCKAVTPPLGNAQSTTTVTLVPEVTSLIKGPDSLIG--- 184
Db 104 FTDGTIRLSRLEDEGVYICGFPATPTGNRESQLNTVMAKPT-NWIEGTQAVLRAKKG 162

Qy 185 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTSPNETATIIISOYKLFPTFRAGR 242
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEAYQIEIRNPNGTIVTISRVLVPSREAHQ 222

Qy 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGNLKNADANPPPFKS 302
Db 223 SLACIVNYHM--DRFKESLTUNVQYEVETIEGFGNWLQRMVDKLTCKADANPPATEY 280

Qy 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGORSQDKVIYISDVFPKQ 362
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPICTRSGQVEVNITEKPRPQ 340

Qy 363 TSIIAVAGAVIGAVLALFIIAIFVTV--LLTPRKKPSYLDKV-IDLPPTHKPPPLYEER 419
Db 341 RLGSAARLLAGVAVFLILVAVTLVFFLVNROOKSPPETDGAGTQDQPLUSQKPEPSRQ 400
Qy 420 SPPLPQKDLFQPEHL--PLQTFKERE 444
```



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; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match      16.9%; Score 458.5; DB 4; Length 479;
Best Local Similarity 30.2%; Pred. No. 1.8e-34;
Matches 121; Conservative 66; Mismatches 160; Indels 53; Gaps 13;

Qy 33 PPTPPPLLLPPLLLPRL-CGALAGPIIVPHVTAVMGKNVSLKCLI---EVNETITQ 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 PPTP-----LLWPLLLLLLLETTGAQDVRVQVLPVVRGQLGGTVLPCHELLPPVGLYISL 67
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 89 ISWEKHGKSS-OTVAVHHPOYGFSGVQGYQG--RVLP-----KNYSINDATITL 135
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 68 VTQRPDAPANQNVAAPHKMGSPSPKPGSERLSFVSAKOSTQDTEAELODATAL 127
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 136 HNIIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLIKGPDLSLIDGNET 188
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 128 HGLTVEDEGNYTCEPATFPKGSVRGWTWLRVIAKPKNOAQAOKVTFPSQDP-----T 178
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 189 VAAICIAATGKPVNAHI-----DWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGR 242
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG----TVTVTSRFTLVPSGRADGV 234
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 243 RITCVVKHPALEKDIRSFILDIQYAPEVSVTYGDNWVGRKGVNLCNADANPPFPKS 302
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 235 TVTCKVEHSEFEPALIPVTLVSRVPEVSIISGDDNMYLGRDTATLSCDVRNPNPTGY 294
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 303 VWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIYISDVFPKQ 362
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 295 DWSTTSGTFTPSAVAQGSQI-VIHAVDSLFTFTVCTVNAVGMGAEQVIFVRETPRAS 353
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 363 TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKRKPS 398
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 354 PRDVGPLWGAAGVGTLLVLLLAGGSLAFILLRVRERKS 393
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 7
US-09-949-016-6278
; Sequence 6278, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6278
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-6278

Query Match      15.0%; Score 406; DB 4; Length 456;
Best Local Similarity 29.4%; Pred. No. 1.5e-29;
Matches 112; Conservative 68; Mismatches 175; Indels 26; Gaps 12;

Qy 22 ASLLGA-GLLQPPPTPPPLLLPRLCGALAGPIIVE--PHVTAVMGKNVSLKC 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AQLGATGNAWAAAAAALLVALLVLSWP---PPGTGDVVVQAPTQVPGFLGDSVTLPC 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 79 LIEVNET-----ITQISWEKHGKSSQTVAVHH---PQYGFSGVQGYQGRVLFKNYSINDA 131
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 118 YLQVFNMEVTHVSQTLTWAR-HGESGMAVPHQTQGFSGYSKSLFEVAARL--GAELRNA 174
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 132 TITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP--TVSLIKGPDLSLIDGNETV 189
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

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US-09-949-016-6278

Query Match      16.9%; Score 458.5; DB 4; Length 479;
Best Local Similarity 30.2%; Pred. No. 1.8e-34;
Matches 121; Conservative 66; Mismatches 160; Indels 53; Gaps 13;

Qy 33 PPTPPPLLLPPLLLPRL-CGALAGPIIVPHVTAVMGKNVSLKCLI---EVNETITQ 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 PPTP-----LLWPLLLLLLLETTGAQDVRVQVLPVVRGQLGGTVLPCHELLPPVGLYISL 67
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 89 ISWEKHGKSS-OTVAVHHPOYGFSGVQGYQG--RVLP-----KNYSINDATITL 135
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 68 VTQRPDAPANQNVAAPHKMGSPSPKPGSERLSFVSAKOSTQDTEAELODATAL 127
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 136 HNIIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLIKGPDLSLIDGNET 188
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 128 HGLTVEDEGNYTCEPATFPKGSVRGWTWLRVIAKPKNOAQAOKVTFPSQDP-----T 178
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 189 VAAICIAATGKPVNAHI-----DWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGR 242
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 179 TVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG----TVTVTSRFTLVPSGRADGV 234
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 243 RITCVVKHPALEKDIRSFILDIQYAPEVSVTYGDNWVGRKGVNLCNADANPPFPKS 302
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 235 TVTCKVEHSEFEPALIPVTLVSRVPEVSIISGDDNMYLGRDTATLSCDVRNPNPTGY 294
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 303 VWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNTSLGQSDQKVIYISDVFPKQ 362
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 295 DWSTTSGTFTPSAVAQGSQI-VIHAVDSLFTFTVCTVNAVGMGAEQVIFVRETPRAS 353
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 363 TSSIA--VAGAVIGAVLALFIIA--IFVTVLLTPRKRKPS 398
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 354 PRDVGPLWGAAGVGTLLVLLLAGGSLAFILLRVRERKS 393
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 8
US-09-949-016-7564
; Sequence 7564, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7564
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-7564

Query Match      15.0%; Score 406; DB 4; Length 456;
Best Local Similarity 29.4%; Pred. No. 1.5e-29;
Matches 112; Conservative 68; Mismatches 175; Indels 26; Gaps 12;

Qy 22 ASLLGA-GLLQPPPTPPPLLLPRLCGALAGPIIVE--PHVTAVMGKNVSLKC 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AQLGATGNAWAAAAAALLVALLVLSWP---PPGTGDVVVQAPTQVPGFLGDSVTLPC 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 79 LIEVNET-----ITQISWEKHGKSSQTVAVHH---PQYGFSGVQGYQGRVLFKNYSINDA 131
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 118 YLQVFNMEVTHVSQTLTWAR-HGESGMAVPHQTQGFSGYSKSLFEVAARL--GAELRNA 174
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 132 TITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP--TVSLIKGPDLSLIDGNETV 189
    :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

```

```
Db 175 SLRPFGLRVEDGNYTCLFTVTPQGSRSVDLWLRVLAQPNTAEVQKVLFT----GAPVP 230
Qy 190 AAICAAATGKPVAHIDWEGDLGEMESTT--TSFPNETATIIISQYKLPFTFARGRRITCV 247
Db 231 MARCVSTGGRPPAQITWHSDLGGMPNTSQVPGFLSGTIVTTSWLIVPSSQVDGKNVTCK 290
Qy 248 VKHPALEKDIRYSFILDIQYAPEVSVTYGDNVFGVRKGVNLCNADANPPPKSVWSRL 307
Db 291 VEHESFEKPOLLTVNLTVYYPVSVISGYDNWNLGQNEATLTCDARSNPETGYNMSTT 350
Qy 308 DGQWPDGLASDNTLHFVHPLTFNYSVYICKVNTNSLGQRSDQKVIIVSDVPPKQTSIA 367
Db 351 MGPLPPFAVAGQAQL--LIRPVDKINTTLCNVNLTALGARQAELTVQKEGPPSEHSGMS 409
Qy 368 VAGAVIGAVLALFIIAIFVTV 388
Db 410 -RNAIIFVLGILVFLILLGI 429

RESULT 9
US-09-949-016-6729
; Sequence 6729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6729
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6729

Query Match 14.9%; Score 402; DB 4; Length 417;
Best Local Similarity 29.3%; Pred. No. 3.1e-29;
Matches 106; Conservative 67; Mismatches 163; Indels 26; Gaps 11;
Qy 44 PLLLLFRLCGAL----AGPIIVE--PHVTAVGKNVSLKCLIEVNET----ITQISWEK 93
Db 9 WPLLLVALLVLSWPPPGTGDVVQAPTQVPQFLGDSVTLPCYLQVPNNVTHVSQLTWTR 68
Qy 94 IHGSSQTVAVH---PQYGFVSQGEYQGRVLFKNYSINDATITLHIGFSDSKYICKA 150
Db 69 -HGSSGMVAFHOTQGPSYSESKLEFVAARL--CAELRNASLRFGLRVEDEGNYTCLF 125
Qy 151 VTFPLGNAQSSTTVTLVLEP--TVSLIKGPDSLDGGNETVAAICIAATGKPVAHIDWEG 208
Db 126 VTFPQGSRSVDIWLRLVLAQPNTAEVQKVLFT----GEPVMAKCVSTGGPPAQITWHS 181
Qy 209 DLGEMESTT--TSFPNETATIIISQYKLPFTFARGRRITCVVKHPALEKDIRYSFILDIQ 266
Db 182 DLGGMPNTSQVPGFLSGTIVTTSWLIVPSSQVDGKNVTCKVEHSEFEKPOLLTVNLTV 241
Qy 267 YAPEVSVTYGDNVFGVRKGVNLCNADANPPPKSVWSRLDGQWPDGLASDNTLHFVH 326
Db 242 YPPEVSVISGYDNWNLGQNEATLTCDARSNPETGYNMSTTGMPLPPFAVAGQAQL--LIR 300
Qy 327 PLTFNYSVGVICKVNTNSLGQRSDQKVIIVSDVPPKQTSIAVAGAVIGAVLALFIIAIFV 386
Db 301 PVDKPINTTLCNVNLTALGARQAELTVQKEGPPSEHSGMS--RNAIIFVLGILVFLILL 359
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Qy 387 TV 388
Db 360 GI 361

RESULT 10
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE REFERENCE: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match 14.8%; Score 400.5; DB 3; Length 408;
Best Local Similarity 30.8%; Pred. No. 4.2e-29;
Matches 123; Conservative 64; Mismatches 167; Indels 45; Gaps 14;
Qy 17 AQLSSASLLGAGLLLOPPTPPPLLLLPPLLLFRLCGAL--AG---PIIVPHVTAWVG 71
Db 2 AQLARAT-----RSPLSWLLLF-----CVALLRKAGGDIRVLVPYNSTGVLG 43
Qy 72 KNYSLKCLIEVNE--TITOISM-EKIHKSOTVAVHHPQVGFVSQGEYQGRVLFKNYSL 128
Db 44 GSTTLHCSLTSENENVTITQITWMKDSGGSHALVAVFHPKKGPNIKSPERVKFLAAQODL 103
Qy 129 NDATITLHNI GFSDGKYICKAVTFPLGNAQSSTTVTLVLEP--TVSLIKGPDSLI--DG 184
Db 104 RNASLAISNLSEDEGIYEQIATFFRGSSTNWLKVAQRPKNATALESPFLIIQD- 162
Qy 185 GNETVAAICIAATGKPVAHIDW----EGDLGEMESTTSPNETATIIISQYKLPFTPAR 240
Db 163 -----VAKCISANGHPGRISWPSNVNGSHRENKE-PGSQPG-TTIVTSYLSMVPESQAD 215
Qy 241 GRRITCVVKHPALEKDIRYSFILDIQYAPE-VSVTYGDNVFGVRKGVNLCNADANPPP 299
Db 216 GKNIITCTVEHESLQELDQLLVTLISQYPYPENSVISGYDNWYVGLTNLTLTCEAHSKPAP 275
Qy 300 FKS--VMSRLDGQWPDGLASDNTLHFVHPLTFNYSVGVICKVNTNSLGQRSDQKVIIVSD 357
Db 276 DMAGYNWSTNGTGFPPNSVKRQGNMLLISTVEDGLNNTVIVCEVTNALSGSGQGVHIIVKE 335
Qy 358 VPFKQTSIIAVAGAVIGAVLALFIIAIFVTVLLTPRKKR 396
Db 336 KPENMQNTRLHLGYIFLIVFLAVVIIIAALYTIIRCCR 374

RESULT 11
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
```

```

; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

Query Match
  11.3%; Score 306.5; DB 4; Length 442;
Best Local Similarity 25.0%; Pred. No. 3.7e-20;
Matches 106; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

QY 8 SPLCPGGKQAQLSSASLILGAGLLLOPPTPPPLLLLPLLLFSLRCLGALAGPIIVEPHVT 67
Db 3 SVLPSGSGCAAAAAPGLRLR-----LLLLFSA---AALPTGQGNLFTKQDVT 53

QY 68 AVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYS 127
Db 54 VIEGEVATISC--QVNKSDSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLNFS 103

QY 128 LNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTVTLVVEPTVSLIK--GPSLIDGNN 186
Db 104 SSELKVSLSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQKDTAVEG-- 159

QY 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMESTTSPNETATIIISQYKLFPTTFRAR 240
Db 160 EELEVNTAWASKPATIRWFKGNTLKGKSEVEESDMY-----TTSQMLKXVHKEDD 214

QY 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTYDGNWVFGKRG--VNLKCNADANPP 298
Db 215 GVPVICQVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274

QY 299 PFKSVWSRLDQWPDGGLASDNLTHFVHPLTFNYSYGVYICKVNSLQORSDDQKVIYISDV 358
Db 275 PVMVTWVRVDDEMPQHAVLSGPNL-FINNLTNDNGTYRCEASNIVGKAHSDYMLYYVDP 333

QY 359 PF-----KOTSSIAVAGAVIGAVLAFIIAIFVTVL 389
Db 334 PTTIPPTTTTTTTTTTTTTTTTTTTTTTIIITDSRAGEEGSIRAVDHAVIGGVAVVVFAMLCCLI 393

QY 390 LTPR 393
Db 394 ILGR 397

RESULT 12
US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match
  11.3%; Score 306.5; DB 4; Length 442;
Best Local Similarity 25.0%; Pred. No. 3.7e-20;
Matches 106; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

QY 8 SPLCPGGKQAQLSSASLILGAGLLLOPPTPPPLLLLPLLLFSLRCLGALAGPIIVEPHVT 67
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QY 68 AVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYS 127
Db 54 VIEGEVATISC--QVNKSDSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLNFS 103

QY 128 LNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSTTVTLVVEPTVSLIK--GPSLIDGNN 186
Db 104 SSELKVSLSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQKDTAVEG-- 159

QY 187 ETVAACIAATGKPVAHIDW-EGDL-----GEMESTTSPNETATIIISQYKLFPTTFRAR 240
Db 160 EELEVNTAWASKPATIRWFKGNTLKGKSEVEESDMY-----TTSQMLKXVHKEDD 214

QY 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTYDGNWVFGKRG--VNLKCNADANPP 298
Db 215 GVPVICQVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274

QY 299 PFKSVWSRLDQWPDGGLASDNLTHFVHPLTFNYSYGVYICKVNSLQORSDDQKVIYISDV 358
Db 275 PVMVTWVRVDDEMPQHAVLSGPNL-FINNLTNDNGTYRCEASNIVGKAHSDYMLYYVDP 333

QY 359 PF-----KOTSSIAVAGAVIGAVLAFIIAIFVTVL 389
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QY 390 LTPR 393
Db 394 ILGR 397

RESULT 13
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Batton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-866-028-61

Query Match
  11.2%; Score 304.5; DB 4; Length 440;
Best Local Similarity 25.2%; Pred. No. 5.6e-20;
Matches 108; Conservative 76; Mismatches 167; Indels 77; Gaps 16;

QY 8 SPLCPGGKQAQLSSASLILGAGLLLOPPTPPPLLLLPLLLFSLRCLGALA---GPIIVE 63
Db 3 SVLPSGSGCAAAAAPGLRLR-----AAPPGLRL---LLLLFS---AALPTGQGNLFT 47

QY 64 PHTVAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLF 123
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Db 98 LNFSSSELKSVLNTVNSISDEGRYFCQLYTD-PQESYTTITVLVPPRNLMIDIQDQAV 155
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Qy 237 RFARRRITCVVHPALEKDIRYSFILDIQYAPESVTVGYDGNWVFGRKG--VNLKCNAD 294
Db 209 KEDDGVPIVCQEHFAVNGNLQTRYLEVQYKQPHIQWYTPLOGLTREGDALETCEAI 268
Qy 295 ANPPFKSVWSRLDQWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQSGQSKVIY 354
Db 269 GRQPQVMVTVRVDDEMPQHAVLSGNL-FINNLNKTDNGTYRCEASNIVGRKHSYMLY 327
Qy 355 ISDVFP-----KQTSSTIAGAVAGIIVAFIIF 385
Db 328 VYDPTTIPPTTTTTTTTTTTTTTTTTTTTTITIDSRAGEGSIKRAVDHAVIGGVAVVVFAML 387
Qy 386 VTLLTPR 393
Db 388 CLLIILGR 395

RESULT 14
US-09-944-457-61
; Sequence 61, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-61

Query Match 11.2%; Score 304.5; DB 4; Length 440;
Best Local Similarity 25.2%; Pred. No. 5.6e-20;
Matches 108; Conservative 76; Mismatches 167; Indels 77; Gaps 16;
Qy 8 SPLCPGGGKQALSSASLIGALLQPPPTPLLLLPFLILFSLRCLGALA----GPIVE 63
Db 3 SVLPSGSQCAAAAA-----AAPGERLL---LLIFS--AALITGQGNLFT 47
Qy 64 PHVTAVMGKNVSLKCLIEVNETITQISWEKTHGKSSQTVAVHHPQYGSVQGYQGRVLF 123
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Db 48 KDVTVIEGEVATISC--QVNSDDSVI--QLLNPNRQTI-----YFRDRPLKDSRFQL 97
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Qy 386 VTLLTPR 393
Db 388 CLLIILGR 395
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RESULT 15
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; TYPE: PRT
; LENGTH: 423
; ORGANISM: Mus musculus
US-09-778-510-22
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Query Match 10.7%; Score 290.5; DB 4; Length 423;
Best Local Similarity 25.7%; Pred. No. 1.1e-18;
Matches 102; Conservative 71; Mismatches 165; Indels 59; Gaps 14;

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Qy 95 HGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFP 154
Db 59 LNPNRQTI-----YFRDRPLKDSRFQLLNFSSSELKVSLSISDEGRYFCQLYTDV 112

Qy 155 LGNAQSSTTVTLVVEPTVSLIK-GPDSLI DGGNETVAAICIAATGKPVAHIDW-EGD--- 209
Db 113 --POESYTTTITVLVPPRNLMIDIOKDTAVEG--EEIEVNTAMASKPATTIRWFKGNEL 168

Qy 210 --LGEMESTTTSFPNETATIIISOYKLFPTFRARGRRITCVVVKHPALEKDIRYSFILDIOY 267
Db 169 KGKSEVEEWSDMY-----TVTSQLMLKVHKKEDDGVPIQVEHPATVGNLQTYRYLEVQY 223

Qy 268 APEYSVTGYDGNWFGVGRKG--VNLKKNADANPPPKSVMSRLDQWPDGGLASDNTLHFV 325
Db 224 KPQVHIQMTYPLQGLTREGDAFELTCEAIGKQPVMVTVVRVDDDEMPQHAVLSGPNL-FI 282
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Qy 326 HPLTFNYSGVYICKVNSLQSDQKVVIYISDVP-----FKQTSI----- 366
Db 283 NNLNKTDNGTYRCEASNIVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTLTIITD 342
Qy 367 -----AVAGAVIGAVLALFIIAIFVTVLLTPR 393
Db 343 SRAGEEGTIGAVDHAIVIGGVAVVVFAMLCLLIILGR 379
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Job time : 23.3581 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 237.135 Seconds
(without alignments)
894.712 Million cell updates/sec

Title: US-09-972-268-12

Perfect score: 2707

Sequence: 1 MARTLRSPICPGGKQAQLS.....KHQNDPKRYIDPREHYV 510

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2693 | 99.5 | 510 | 10 | Sequence 12, Appl |
| 3 | 2679 | 99.0 | 504 | 10 | Sequence 10, Appl |
| 4 | 2388 | 88.2 | 510 | 10 | Sequence 8, Appl |
| 5 | 2388 | 88.2 | 510 | 10 | Sequence 4, Appl |
| 6 | 2257 | 83.4 | 437 | 10 | US-09-972-268-18 |
| 7 | 2107 | 77.8 | 438 | 10 | US-09-972-268-31 |
| 8 | 2107 | 77.8 | 438 | 10 | US-09-959-845-6 |
| 9 | 1920.5 | 70.9 | 549 | 10 | US-09-972-268-19 |
| 10 | 1920.5 | 70.9 | 549 | 14 | US-09-972-268-6 |
| 11 | 1914 | 70.7 | 595 | 10 | US-10-161-572-45 |
| | | | | | US-09-972-268-14 |

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|----|--------|------|-----|----|--------------------|
| 12 | 1912 | 70.6 | 397 | 10 | US-09-972-268-16 |
| 13 | 1906.5 | 70.4 | 549 | 10 | US-09-972-268-4 |
| 14 | 1885.5 | 69.7 | 542 | 10 | US-09-972-268-2 |
| 15 | 1885.5 | 69.7 | 634 | 10 | US-09-972-268-13 |
| 16 | 1880 | 69.4 | 426 | 10 | US-09-972-268-15 |
| 17 | 1819.5 | 67.2 | 549 | 10 | US-09-959-845-2 |
| 18 | 1819.5 | 67.2 | 549 | 10 | US-09-972-268-17 |
| 19 | 588 | 21.7 | 514 | 14 | US-10-161-572-60 |
| 20 | 588 | 21.7 | 517 | 10 | US-09-972-268-20 |
| 21 | 587.5 | 21.7 | 458 | 10 | US-09-972-268-21 |
| 22 | 565.5 | 20.9 | 518 | 9 | US-09-919-172-20 |
| 23 | 565.5 | 20.9 | 518 | 16 | US-10-752-986-20 |
| 24 | 540 | 19.9 | 530 | 18 | US-10-631-467-1474 |
| 25 | 538.5 | 19.9 | 485 | 15 | US-10-422-571-15 |
| 26 | 538.5 | 19.9 | 485 | 15 | US-10-422-571-33 |
| 27 | 538.5 | 19.9 | 485 | 15 | US-10-422-571-114 |
| 28 | 538.5 | 19.9 | 485 | 15 | US-10-422-571-116 |
| 29 | 538.5 | 19.9 | 485 | 15 | US-10-422-571-129 |
| 30 | 538.5 | 19.9 | 497 | 10 | US-09-972-268-37 |
| 31 | 537 | 19.8 | 498 | 10 | US-09-972-268-39 |
| 32 | 527.5 | 19.5 | 510 | 15 | US-10-422-571-5 |
| 33 | 527.5 | 19.5 | 510 | 15 | US-10-422-571-31 |
| 34 | 527 | 19.5 | 538 | 10 | US-09-972-268-23 |
| 35 | 527 | 19.5 | 538 | 10 | US-09-984-130-138 |
| 36 | 527 | 19.5 | 538 | 10 | US-09-836-353A-138 |
| 37 | 527 | 19.5 | 538 | 14 | US-10-161-572-61 |
| 38 | 527 | 19.5 | 538 | 15 | US-10-411-010-17 |
| 39 | 527 | 19.5 | 538 | 17 | US-10-953-264-17 |
| 40 | 524 | 19.4 | 510 | 15 | US-10-422-571-25 |
| 41 | 524 | 19.4 | 510 | 15 | US-10-422-571-36 |
| 42 | 523.5 | 19.3 | 510 | 14 | US-09-766-511B-33 |
| 43 | 523.5 | 19.3 | 510 | 14 | US-10-241-220-94 |
| 44 | 523.5 | 19.3 | 510 | 15 | US-10-295-027-66 |
| 45 | 523.5 | 19.3 | 510 | 15 | US-10-173-999-76 |

ALIGNMENTS

RESULT 1

US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

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| Query Match | 100.0%; | Score 2707; | DB 10; | Length 510; |
| Best Local Similarity | 100.0%; | Pred. No. 7.5e-198; | | |
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| | | | Indels | 0; |
| | | | Gaps | 0; |
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Qy 181 LIDGNETVAAICIAATGKPVVAHIIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAAICIAATGKPVVAHIIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Qy 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLCNADANPPPF 300
Qy 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDOKVYIISDVPP 360
Db 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDOKVYIISDVPP 360
Qy 361 KOTSSIAVAGAVIGAVLALFIATFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KOTSSIAVAGAVIGAVLALFIATFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420
Qy 421 PPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQOMYPLYN 480
Db 421 PPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQOMYPLYN 480
Qy 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510
Db 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510
RESULT 2
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10
Query Match 99.5%; Score 2693; DB 10; Length 510;
Best Local Similarity 99.6%; Pred. No. 8.8e-197;
Matches 508; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MARTLRSPICPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFSLRCLGALAGPI 60
Db 1 MARTPGSPICPGGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFSLRCLGALAGPI 60
Qy 61 IVEPHVTAVGKGNVSKLCLEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
Db 61 IVEPHVTAVGKGNVSKLCLEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
Qy 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAAICIAATGKPVVAHIIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAAICIAATGKPVVAHIIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Qy 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLCNADANPPPF 300
Qy 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDOKVYIISDVPP 360
Db 301 KSVWSRLDGGWPDLGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDOKVYIISDVPP 360
Qy 361 KOTSSIAVAGAVIGAVLALFIATFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KOTSSIAVAGAVIGAVLALFIATFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLYEERS 420
Qy 421 PPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQOMYPLYN 480
Db 421 PPLPQKDLFQPEHLPLQTFQKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQOMYPLYN 480
Qy 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510
Db 481 QMCYQDRSPGKHQNNNDPKRVYIDPREHYV 510
RESULT 3
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8
Query Match 99.0%; Score 2679; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 1e-195;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PSLPCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFSLRCLGALAGPIIVEPHV 66
Db 1 PSLPCPGGKAQLSSASLLGAGLLQLPPTPPPLLLLPFLLLFSLRCLGALAGPIIVEPHV 60
Qy 67 TAVWGNVSKLCLEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNY 126
Db 61 TAVWGNVSKLCLEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNY 120
Qy 127 SLMDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGN 186
Db 121 SLMDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGN 180
Qy 187 ETVAATCIAATGKPVVAHIIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRARGRITC 246
Db 181 ETVAATCIAATGKPVVAHIIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRARGRITC 240
Qy 247 VVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLCNADANPPPFKSVWSR 306
Db 241 VVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLCNADANPPPFKSVWSR 300


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Qy 307 LDGQWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVYISDVPPKQTSSI 366
Db 301 LDGQWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVYISDVPPKQTSSI 360
Qy 367 AVAGAVIGAVLALFIIAIVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERSPPLPQK 426
Db 361 AVAGAVIGAVLALFIIAIVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERSPPLPQK 420
Qy 427 DLFOPEHLPLQTOFKEREVGNLQHSNGLNSRSDFYEDENPVGSDGIQOMYPLYNQMCYQD 486
Db 421 DLFOPEHLPLQTOFKEREVGNLQHSNGLNSRSDFYEDENPVGSDGIQOMYPLYNQMCYQD 480
Qy 487 RSPCKHQHNDPKRVIYIDPREHYV 510
Db 481 RSPCKHQHNDPKRVIYIDPREHYV 504

RESULT 4
US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4

Query Match 88.2%; Score 2388; DB 10; Length 510;
Best Local Similarity 88.8%; Pred. No. 1.6e-173;
Matches 454; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

Qy 1 MARTLRSPCLPCGGKQAQLSSASLLGAGLLIOPPTPPPLLLLLPPLLLFSLRCGALAGPI 60
Db 1 MARTPGPAPLPCGGKQAQLSSAFPAPAGLLLPATPPPLLLLLPPLLLFSLRCGALAGSI 60

Qy 61 IVEPHVTAVMGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHQYGFSGVQGYQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNNTITQISWEKIHGKSTQTVAVHHQYGFSGVQGYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGSDS 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGSDS 180

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAACVAATGKPAQIDWEGDLGEMESTTSPNETATIVSQYKLPPTFRAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFF 300

Qy 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVYISDVPPF 360
Db 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVYISDVPPF 360

Qy 361 KOTSSIAVAGAVIGAVLALFIIAIVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERS 479
Db 361 KOTSSIAVAGAVIGAVLALFIIAIVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERS 480

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Db 361 TOTSSIAVAGAVIGAVLALFIIITVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERI 420
Qy 421 PPLPQKDLF-QPEHLPLQTOFKEREVGNLQHSNGLNSRSDFYEDENPVGSDGIQOMYPLY 479
Db 421 PSLPQKDLGQTEHLPLQTOFKKEGAGGLQPSNGPISRRFDYEDESTMQEDGTQRMCPPLY 480
Qy 480 NOMCYQDRSPGKHQHNDPKRVIYIDPREHYV 510
Db 481 SQMCHQDRSPRQHHPRN-PERLYINPREHYV 510

RESULT 5
US-09-972-268-18
; Sequence 18, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 510
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-18

Query Match 88.2%; Score 2388; DB 10; Length 510;
Best Local Similarity 88.8%; Pred. No. 1.6e-173;
Matches 454; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

Qy 1 MARTLRSPCLPCGGKQAQLSSASLLGAGLLIOPPTPPPLLLLLPPLLLFSLRCGALAGPI 60
Db 1 MARTPGPAPLPCGGKQAQLSSAFPAPAGLLLPATPPPLLLLLPPLLLFSLRCGALAGSI 60

Qy 61 IVEPHVTAVMGKNSVLSKCLIEVNNTITQISWEKIHGKSSQTVAVHHQYGFSGVQGYQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNNTITQISWEKIHGKSTQTVAVHHQYGFSGVQGYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGSDS 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGSDS 180

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFRAR 240
Db 181 LIDGNETVAACVAATGKPAQIDWEGDLGEMESTTSPNETATIVSQYKLPPTFRAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFF 300

Qy 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVYISDVPPF 360
Db 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVYISDVPPF 360

Qy 361 KOTSSIAVAGAVIGAVLALFIIAIVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 KOTSSIAVAGAVIGAVLALFIIAIVTVLLTPRKRSYLDKVIDLPPTHKPPPLYEERS 420

Qy 421 PPLPQKDLF-QPEHLPLQTOFKEREVGNLQHSNGLNSRSDFYEDENPVGSDGIQOMYPLY 479
Db 421 PSLPQKDLGQTEHLPLQTOFKKEGAGGLQPSNGPISRRFDYEDESTMQEDGTQRMCPPLY 480
Qy 480 NOMCYQDRSPGKHQHNDPKRVIYIDPREHYV 510

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Db      481 SOMCHQDRSPROHPRN-PERLYNPREHYV 510

RESULT 6
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match      83.4%; Score 2257; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.3e-163;
Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARTLRPSPLCPGGKKAQLSSASLLGAGLLLOPPTPPPLLLLLFPPLLSRLCGALAGPI 60
Db      1 MARTLRPSPLCPGGKKAQLSSASLLGAGLLLOPPTPPPLLLLLFPPLLSRLCGALAGPI 60

QY      61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
Db      61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120

QY      121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSQTVVLEPTVSLIKGPD 180
Db      121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSQTVVLEPTVSLIKGPD 180

QY      181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db      181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240

QY      241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300
Db      241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300

QY      301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
Db      301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360

QY      361 KQTSSIAVAGAVICAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db      361 KQTSSIAVAGAVICAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420

QY      421 PPLPQKDLFQ 430
Db      421 PPLPQKDLFQ 430

RESULT 7
US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiyuki TAKAI
; APPLICANT: Hiroaki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI

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; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

Query Match      77.8%; Score 2107; DB 10; Length 438;
Best Local Similarity 93.2%; Pred. No. 3.7e-152;
Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY      1 MARTLRPSPLCPGGKKAQLSSASLLGAGLLLOPPTPPPLLLLLFPPLLSRLCGALAGPI 60
Db      1 MARTLRPSPLCPGGKKAQLSSASLLGAGLLLOPPTPPPLLLLLFPPLLSRLCGALAGSI 60

QY      61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120
Db      61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGR 120

QY      121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSQTVVLEPTVSLIKGPD 180
Db      121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSQTVVLEPTVSLIKGPD 180

QY      181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db      181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240

QY      241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300
Db      241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPF 300

QY      301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360
Db      301 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPF 360

QY      361 KQTSSIAVAGAVICAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db      361 KQTSSIAVAGAVICAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERI 420

QY      421 PPLPQKDL 428
Db      421 PSLPQKDL 428

RESULT 8
US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 438

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; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

Query Match      77.8%; Score 2107; DB 10; Length 438;
Best Local Similarity 93.2%; Pred. No. 3.7e-152;
Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGGKQAQLSSASLIGAGLLIQPTTPTPLLLLPFLLLFSLRCGALAGPI 60
Db 1 MARTLRPSPLCPGGKQAQLSSASLIGAGLLIQPTTPTPLLLLPFLLLFSLRCGALAGSI 60

Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITOI SWEKIHGKSSQTVAVHHPOYGFSGVOEQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITOI SWEKIHGKSSQTVAVHHPOYGFSGVOEQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPD 180

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTTPAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTTTPAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300

Qy 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSVYICKVTNSLGQSDQKVIYISDVP 359
Db 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSVYICKVTNSLGQSDQKVIYISDVP 359

Qy 360 -----FKQTSSIAVAGAVICAVLALFIIA 383
Db 361 TTTLQPTIOWHPSTADIEDLATEPKLPPLSTLTATIKDDTIATIIASVVGALFIVLVS 420

Qy 384 IFVTVLLTPRK--RPSYLDKVIDLPETHK-----PPPLYEERSPELP 424
Db 421 VLAGIFCVRRTTRFGDYFANKY--IPPSDMQKESQIDVLQODELSDVPDSVKKNKQPV- 478

Qy 425 QKOLFPQEHIL--PLQTFQKEREVGNLQHSNLSRSDYEDENPVGEGDIOQMYPLXNQ 482
Db 479 -NNLRKDYLEEPKQW-----NNVENLRF-ERPMDYEDLKWGMKFVSD----- 523

Qy 483 CYQDRSPGKHQNNDPKRV-----YIDPREHYV 510
Db 524 -----EHDYDENEEDDLVSHVDGVSISRREYV 549

RESULT 10
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match      70.9%; Score 1920.5; DB 14; Length 549;
Best Local Similarity 67.9%; Pred. No. 8.5e-138;
Matches 390; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

Qy 1 MARTLRPSPLCPGGKQAQLSSASLIGAGLLIQPTTPTPLLLLPFLLLFSLRCGALAGPI 60
Db 1 MARTLRPSPLCPGGKQAQLSSASLIGAGLLIQPTTPTPLLLLPFLLLFSLRCGALAGPI 60
```

QY 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 Db 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 QY 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDADANPPPF 300
 Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDADANPPPF 300
 QY 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVYIISDVP 359
 Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVYIISDVP 360
 QY 360 -----FKQTSSIAVAGAVIGALVAFIIA 383
 Db 361 TTTLOPTIONHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
 QY 384 IFVTLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPPLP 424
 Db 421 VLAGIFCYRRRTFRGDFYFKNY-IPESDMQKESQIDVLOODELDSYDPSVKKENKPV- 478
 QY 425 QKOLFQPEHL--PLQTOFKEREVGNLQHSNLSRSDYEDENPNVGSDEGIQQMYPLYNQM 482
 Db 479 -NNLRKDYLEEPKQW-----NNVENLNR-ERPMDYEDLKMGMKFVSD----- 523
 QY 483 CYQDRSGKHKQNDPRV-----YIDPREHYV 510
 Db 524 -----EHDYENEDDLVSHVDGVSISRREYV 549
 RESULT 11
 US-09-972-268-14
 ; Sequence 14, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanslow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 595
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
 US-09-972-268-14
 Query Match 70.7%; Score 1914; DB 10; Length 595;
 Best Local Similarity 86.3%; Pred. No. 3e-137;
 Matches 373; Conservative 3; Mismatches 18; Indels 38; Gaps 2;
 QY 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLLOPPTPPLLLLPPLLLFSLRCLGALAGPI 60
 Db 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLLOPPTPPLLLLPPLLLFSLRCLGALAGPI 60
 QY 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 Db 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 QY 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDADANPPPF 300
 Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDADANPPPF 300
 QY 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVYIISDVP 359
 Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVYIISDVP 360
 QY 360 -----FKQTSSIAVAGAVIGALVAFIIA 383
 Db 361 TTTLOPTIONHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFVLVS 420
 QY 384 IFVTLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPPLP 424
 Db 421 VLAGIFCYRRRTFRGDFYFKNY-IPESDMQKESQIDVLOODELDSYDPSVKKENKPV- 478
 QY 425 QKOLFQPEHL--PLQTOFKEREVGNLQHSNLSRSDYEDENPNVGSDEGIQQMYPLYNQM 482
 Db 479 -NNLRKDYLEEPKQW-----NNVENLNR-ERPMDYEDLKMGMKFVSD----- 523
 QY 483 CYQDRSGKHKQNDPRV-----YIDPREHYV 510
 Db 524 -----EHDYENEDDLVSHVDGVSISRREYV 549

Db 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 QY 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 QY 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDADANPPPF 300
 Db 241 GRITCVVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDADANPPPF 300
 QY 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVYIISDVP 360
 Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVYIISDVP 360
 QY 361 KOTSSIAVAGAVIGALVAFIIAIFVTLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS 420
 Db 361 KQTSSR-----CDK-----THTCPCPAPEA 382
 QY 421 PPLPQKDLFQPE 432
 Db 383 EGAPSVFLFPFK 394
 RESULT 12
 US-09-972-268-16
 ; Sequence 16, Application US/09972268
 ; Publication No. US20030044893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter R.
 ; APPLICANT: Fanslow, William C.
 ; APPLICANT: Lofton, Timothy E.
 ; APPLICANT: Sorensen, Eric A.
 ; APPLICANT: Youakim, Adel
 ; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
 ; FILE REFERENCE: 3101-A
 ; CURRENT APPLICATION NUMBER: US/09/972,268
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,557
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
 US-09-972-268-16
 Query Match 70.6%; Score 1912; DB 10; Length 387;
 Best Local Similarity 99.5%; Pred. No. 2.4e-137;
 Matches 363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLLOPPTPPLLLLPPLLLFSLRCLGALAGPI 60
 Db 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLLOPPTPPLLLLPPLLLFSLRCLGALAGPI 60
 QY 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 Db 61 IVEPHVTAVGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFSGVQYQGR 120
 QY 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNVSLNDATTTLHNIGFSDSGKYICKAVTFFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
 Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240

Qy 241 GRRITCVVKKHPEKDIRYSFILDIOVAPEVSVTGYDGNWFWGRKGNLKNADANPPPP 300
Db 241 GRRITCVVKKHPEKDIRYSFILDIOVAPEVSVTGYDGNWFWGRKGNLKNADANPPPP 300
Qy 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVPF 360
Db 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVPF 360
Qy 361 KQTSS 365
Db 361 KQTSS 365

RESULT 13

US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 70.4%; Score 1906.5; DB 10; Length 549;
Best Local Similarity 67.6%; Pred. No. 1e-136;
Matches 388; Conservative 33; Mismatches 64; Indels 89; Gaps 10;

Qy 1 MARTLRPSLPCGGGKAQLSSASLLGAGLLLOPPTPPPLLLPFLLSRLCGALAGPI 60
Db 1 MARTPGSPSLPCGGGKAQLSSASLLGAGLLLOPPTPPPLLLPFLLSRLCGALAGPI 60
Qy 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGR 120
Qy 121 VLFKNYSNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAICIAATGKPAHIDWEGDLGEMESTTSPFNATATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAICIAATGKPAHIDWEGDLGEMESTTSPFNATATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVKKHPEKDIRYSFILDIOVAPEVSVTGYDGNWFWGRKGNLKNADANPPPP 300
Db 241 GRRITCVVKKHPEKDIRYSFILDIOVAPEVSVTGYDGNWFWGRKGNLKNADANPPPP 300
Qy 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVP 359
Db 301 KSVMSRLDGOWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVP 360
Qy 360 -----FKQTSSIAVAGAVIGALVAFIA 383
Db 361 TTTILOPTIOWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
Qy 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 424

Db 421 VLAGIFCYRRRTFRGDIYFAKNY-IPPSDMQKESQIDVLQODELSDSYDPSVKKNKRPV- 478
Qy 425 QKOLFQPEHL--PLQTOFKEREYGNLQHSNLSRSPDYEDENPVGEGDGIQMYPLYNQM 482
Db 479 --NNLIRKDYLEPEKQW-----NNVENLRF-ERPMDYVEDLKMGMKFVSD----- 523
Qy 483 CYQDRSPGKHQNDPKRV-----YIDPREHYV 510
Db 524 -----EHYDENEDDLVSHVDGVSIRREWYV 549

RESULT 14

US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 69.7%; Score 1885.5; DB 10; Length 542;
Best Local Similarity 67.5%; Pred. No. 3.9e-135;
Matches 383; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

Qy 8 SPLPCGGGKAQLSSASLLGAGLLLOPPTPPPLLLPFLLSRLCGALAGPIIVEPHVT 67
Db 1 SPLPCGGGKAQLSSASLLGAGLLLOPPTPPPLLLPFLLSRLCGALAGPIIVEPHVT 60
Qy 68 AVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGRVLFKNYS 127
Db 61 AVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQYQGRVLFKNYS 120
Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 187
Db 121 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 188 TVAAICIAATGKPAHIDWEGDLGEMESTTSPFNATATIIISQYKLPFTRFAR 247
Db 181 TVAAICIAATGKPAHIDWEGDLGEMESTTSPFNATATIIISQYKLPFTRFAR 240
Qy 248 VKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFWGRKGNLKNADANPPPKSVMSRL 307
Db 241 VKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFWGRKGNLKNADANPPPKSVMSRL 300
Qy 308 DGQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVP----- 359
Db 301 DGQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVP----- 360
Qy 360 -----FKQTSSIAVAGAVIGALVAFIA 390
Db 361 IOWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
Qy 391 TPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLP 431
Db 421 YRRRTFRGDIYFAKNY-IPPSDMQKESQIDVLQODELSDSYDPSVKKNKRPV--NNLIRK 477
Qy 432 EHL--PLQTOFKEREYGNLQHSNLSRSPDYEDENPVGEGDGIQMYPLYNQM 489

```

Db 478 DYLEBEKTOW-----NNVENLNRFP-ERPMDYYEDLKMGMKFVSD----- 516
QY 490 GKHHQNNDPKRV-----YIDPREHYV 510
Db 517 -EYDENEDDLVSHVDGVSISRREWYV 542

RESULT 15
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 69.7%; Score 1885.5; DB 10; Length 634;
Best Local Similarity 83.9%; Pred. No. 4.8e-135;
Matches 371; Conservative 7; Mismatches 45; Indels 19; Gaps 2;

QY 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLQLPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
Db 1 MARTPGSPPLCPGGKQAQLSSASLLGAGLLQLPPTPPPLLLLPPLLLFSLRLCGALAGPI 60
QY 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGDS 180
Db 121 VLFKNYSLNDATITLHNIGFSDGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGDS 180
QY 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
QY 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
QY 301 KSVWSRLDGOWPDGLLASDNTLHFVPLTFNYSGVYICKVTNSLQGRSDOKVIYISDVPF 360
Db 301 KSVWSRLDGOWPDGLLASDNTLHFVPLTFNYSGVYICKVTNSLQGRSDOKVIYISDVPT 360
QY 361 KQTSSIAVAGAVIGALALFIIAIVTVLLTPRKRPSYLDKVIDL-----PPTH 410
Db 361 TTT-----LQPTIQWHPSTADIEDLATEPKKLPPLSLTATIKDDTIATRSCKKTH 411
QY 411 KPPLYEERSPPLPKDLFQPE 432
Db 412 TCPPCPAEAEAGAPSVFLFPEK 433
```

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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 72.1777 Seconds
(without alignments)
2341.642 Million cell updates/sec

Title: US-09-972-268-31

Perfect score: 2299

Sequence: 1 MATLRSPPLCPGGGKAQLS.....ERSPPLPQKDLFQVCVHEYT 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 2299 | 100.0 | 437 | 5 | Aae23299 Human nec |
| 2 | 2257 | 98.2 | 510 | 5 | Aae23286 Human nec |
| 3 | 2243 | 97.6 | 510 | 5 | Aae23285 Mouse nec |
| 4 | 2229 | 97.0 | 504 | 5 | Aae23284 Human del |
| 5 | 2108 | 91.7 | 510 | 4 | Aag63983 Amino aci |
| 6 | 2108 | 91.7 | 510 | 5 | Aae23292 Mouse nec |
| 7 | 2107 | 91.6 | 438 | 4 | Aag63984 Amino aci |
| 8 | 2107 | 91.6 | 438 | 5 | Aae23293 Mouse nec |
| 9 | 1912 | 83.2 | 387 | 5 | Aae23290 Human nec |
| 10 | 1912 | 83.2 | 595 | 5 | Aae23288 Human nec |
| 11 | 1902.5 | 82.8 | 549 | 5 | Aae23283 Human nec |
| 12 | 1902.5 | 82.8 | 549 | 6 | Aaj20222 Human IG |
| 13 | 1902.5 | 82.8 | 549 | 8 | Adr66369 Human pro |
| 14 | 1902.5 | 82.8 | 549 | 8 | Adr66711 Human pro |
| 15 | 1888.5 | 82.1 | 549 | 5 | Aae23282 Mouse nec |
| 16 | 1879 | 81.7 | 634 | 5 | Aae23287 Human nec |
| 17 | 1878 | 81.7 | 426 | 5 | Aae23289 Human nec |
| 18 | 1867.5 | 81.2 | 542 | 5 | Aae23281 Human del |
| 19 | 1863.5 | 81.1 | 555 | 4 | Aam39143 Human pol |
| 20 | 1803 | 78.4 | 549 | 4 | Aag63982 Amino aci |
| 21 | 1803 | 78.4 | 549 | 4 | Aag63985 Amino aci |
| 22 | 1803 | 78.4 | 549 | 5 | Aae23291 Mouse nec |
| 23 | 1785.5 | 77.7 | 559 | 4 | Aam40929 Human pol |
| 24 | 1235 | 53.7 | 267 | 4 | Aam93536 Human pol |
| 25 | 1235 | 53.7 | 267 | 8 | Adl31248 Human pro |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 26 | 628.5 | 27.3 | 305 | 5 | ADR41425 | Adr41425 Human CD- |
| 27 | 581 | 25.3 | 458 | 5 | AAE23295 | Aae23295 Human nec |
| 28 | 566.5 | 24.6 | 514 | 6 | ABJ20237 | Abj20237 Human IG |
| 29 | 566.5 | 24.6 | 517 | 3 | AAy32390 | Aay32390 Herpesvir |
| 30 | 566.5 | 24.6 | 517 | 5 | AAE23294 | Aae23294 Human nec |
| 31 | 544 | 23.7 | 518 | 5 | ABG77170 | Abg77170 Prostate |
| 32 | 543 | 23.6 | 580 | 8 | ADO47877 | Ado47877 Alpha-Her |
| 33 | 543 | 23.6 | 581 | 8 | ADP03590 | Adp03590 Infection |
| 34 | 542 | 23.6 | 578 | 8 | ADP03592 | Adp03592 Infection |
| 35 | 530.5 | 23.1 | 352 | 8 | ABM83397 | Abm83397 Human dia |
| 36 | 530.5 | 23.1 | 353 | 8 | ABM83396 | Abm83396 Human dia |
| 37 | 530.5 | 23.1 | 353 | 8 | ABM83395 | Abm83395 Human dia |
| 38 | 526 | 22.9 | 510 | 8 | ADK83174 | Adk83174 Human 191 |
| 39 | 526 | 22.9 | 510 | 8 | ADK83200 | Adk83200 Human 191 |
| 40 | 522 | 22.7 | 485 | 8 | ADK83283 | Adk83283 Human 191 |
| 41 | 522 | 22.7 | 485 | 8 | ADK83298 | Adk83298 Human 191 |
| 42 | 522 | 22.7 | 485 | 8 | ADK83184 | Adk83184 Human 191 |
| 43 | 522 | 22.7 | 485 | 8 | ADK83202 | Adk83202 Human 191 |
| 44 | 522 | 22.7 | 485 | 8 | ADK83285 | Adk83285 Human 191 |
| 45 | 522 | 22.7 | 497 | 5 | AAE23303 | Aae23303 Human nec |

ALIGNMENTS

RESULT 1

AAE23299
ID AAE23299 standard; protein; 437 AA.

XX AAE23299;
AC AAE23299;

XX
DT 27-AUG-2002 (first entry)
XX

XX Human nectin-3gamma protein.
DE
XX

XX Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX Homo sapiens.
OS

XX WO200228902-A2.
FN

XX 11-APR-2002.
PD

XX 05-OCT-2001; 2001WO-US031392.
PF

XX 05-OCT-2000; 2000US-0238557P.
PR

XX (IMMV) IMMUNEX CORP.
PA

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI

XX WPI; 2002-426103/45.
DR

XX N-PSDB; AAD37450.
DR

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

XX Claim 1; Page 125-126; 141pp; English.
PS

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

| | | |
|----------|---|--|
| CC | asthma, allergy, allograft rejection, metastasis of cancer cells, | |
| CC | paracellular transport disorders such as magnesium transport defects in | |
| CC | the kidney or inflammatory bowel disease. Nectin DNA is also useful for | |
| CC | inhibiting angiogenesis in a mammal and treating endothelial migration, | |
| CC | proliferation or angiogenic condition of a tissue or a subject, such as | |
| CC | ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, | |
| CC | stroke, restenosis, tumour growth and treating herpesvirus infection. | |
| CC | Nectin is also useful for modulating proliferation or migration of an | |
| CC | endothelial cell, an epithelial cell or a smooth muscle cell (vascular | |
| CC | smooth muscle cell). The present sequence is human nectin-3gamma protein. | |
| CC | Human nectin-3gamma gene is located on chromosome 3 | |
| XX | | |
| SQ | Sequence 437 AA; | |
| | Query Match 100.0%; Score 2299; DB 5; Length 437; | |
| | Best Local Similarity 100.0%; Pred. No. 1.6e-180; | |
| | Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 MARTLRPSPLCPGGKAQLSSALLGAGLLQLQPTPPPLLLFPPLLLFSRLCGALAGPI 60 | |
| DB | 1 MARTLRPSPLCPGGKAQLSSALLGAGLLQLQPTPPPLLLFPPLLLFSRLCGALAGPI 60 | |
| QY | 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVHHPQYGFVSQGEYQGR 120 | |
| DB | 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVHHPQYGFVSQGEYQGR 120 | |
| QY | 121 VLPKNYSLNDAITLHNIGSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180 | |
| DB | 121 VLPKNYSLNDAITLHNIGSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180 | |
| QY | 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240 | |
| DB | 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240 | |
| QY | 241 GRITCVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFGVKGNLKNADANPPPF 300 | |
| DB | 241 GRITCVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFGVKGNLKNADANPPPF 300 | |
| QY | 301 KSWSRLDGOWPGLLASDNLHFVHPLTFNYSGVICKVTNSLGQSDQKVIYISDVPF 360 | |
| DB | 301 KSWSRLDGOWPGLLASDNLHFVHPLTFNYSGVICKVTNSLGQSDQKVIYISDVPF 360 | |
| QY | 361 KQTSSIAVAGAVIGAVLALFIIIFVTVLLTPRKRPYSLDKVIDLPPTHKPPPLYEERS 420 | |
| DB | 361 KQTSSIAVAGAVIGAVLALFIIIFVTVLLTPRKRPYSLDKVIDLPPTHKPPPLYEERS 420 | |
| QY | 421 PPLPQKDLFQVCVHEYT 437 | |
| DB | 421 PPLPQKDLFQVCVHEYT 437 | |
| RESULT 2 | | |
| ID | AAE23286 | |
| AC | AAE23286 standard; protein; 510 AA. | |
| XX | | |
| XX | AAE23286; | |
| XX | | |
| DT | 27-AUG-2002 (first entry) | |
| DE | Human nectin-3beta protein. | |
| XX | | |
| KW | Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; | |
| KW | paracellular transport disorder; kidney; diabetic retinopathy; allergy; | |
| KW | allograft rejection; metastasis; restenosis; inflammatory bowel disease; | |
| KW | oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; | |
| KW | stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| XX | | |
| Key | Location/Qualifiers | |
| FT | Modified-site 73 | |
| FT | /note= "N-glycosylated" | |
| FT | | |
| FT | Domain 74. .152 | |

| | | |
|----|---|--|
| FT | Modified-site | /note= "Extracellular Ig domain" |
| FT | 83 | |
| FT | Modified-site | /note= "N-glycosylated" |
| FT | 125 | |
| FT | Modified-site | /note= "N-glycosylated" |
| FT | 186 | |
| FT | Domain | /note= "N-glycosylated" |
| FT | 189. .250 | |
| FT | Modified-site | /note= "Extracellular Ig domain" |
| FT | 222 | |
| FT | Domain | /note= "N-glycosylated" |
| FT | 287. .342 | |
| FT | Modified-site | /note= "N-glycosylated" |
| FT | 331 | |
| FT | Domain | /note= "Extracellular Ig domain" |
| FT | 386. .510 | |
| FT | | /note= "Intracellular C-terminal domain" |
| XX | | |
| XX | WO200228902-A2. | |
| XX | 11-APR-2002. | |
| XX | | |
| PF | 05-OCT-2001; 2001WO-US031392. | |
| XX | | |
| PR | 05-OCT-2000; 2000US-0238557P. | |
| XX | (IMMV) IMMUNEX CORP. | |
| PA | | |
| XX | Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A; | |
| PI | | |
| XX | WPI; 2002-426103/45. | |
| DR | N-PSDB; AAD37445. | |
| XX | | |
| PT | Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, | |
| PT | useful for treating or preventing heart failure, malaria, | |
| PT | glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, | |
| PT | sepsis, stroke. | |
| XX | | |
| PS | Claim 1; Page 98-99; 141pp; English. | |
| XX | | |
| CC | The invention relates to a substantially purified nectin3alpha, beta, | |
| CC | gamma and nectin-4 polypeptides and their corresponding polynucleotides. | |
| CC | Nectin DNA and protein are useful for treating a disease associated with | |
| CC | cell adhesion activity, adherens junction formation activity, epithelial | |
| CC | or endothelial barrier function activity, endothelial proliferation or | |
| CC | migration activity, viral polypeptide binding activity. The epithelial or | |
| CC | endothelial barrier function disorder which is treated by the above | |
| CC | mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, | |
| CC | asthma, allergy, allograft rejection, metastasis of cancer cells, | |
| CC | paracellular transport disorders such as magnesium transport defects in | |
| CC | the kidney or inflammatory bowel disease. Nectin DNA is also useful for | |
| CC | proliferation or angiogenic condition of a tissue or a subject, such as | |
| CC | ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, | |
| CC | stroke, restenosis, tumour growth and treating herpesvirus infection. | |
| CC | Nectin is also useful for modulating proliferation or migration of an | |
| CC | endothelial cell, an epithelial cell or a smooth muscle cell (vascular | |
| CC | smooth muscle cell). The present sequence is human nectin-3beta protein. | |
| CC | Human nectin-3beta gene is located on chromosome 3 | |
| XX | | |
| SQ | Sequence 510 AA; | |
| | Query Match 98.2%; Score 2257; DB 5; Length 510; | |
| | Best Local Similarity 100.0%; Pred. No. 5.7e-177; | |
| | Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 MARTLRPSPLCPGGKAQLSSALLGAGLLQLQPTPPPLLLFPPLLLFSRLCGALAGPI 60 | |
| DB | 1 MARTLRPSPLCPGGKAQLSSALLGAGLLQLQPTPPPLLLFPPLLLFSRLCGALAGPI 60 | |
| QY | 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVHHPQYGFVSQGEYQGR 120 | |
| DB | 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVHHPQYGFVSQGEYQGR 120 | |

Qy 121 VLFKNSLNDATITLHNIGSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db |||||
 Qy 121 VLFKNSLNDATITLHNIGSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
 Db |||||
 Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240
 Db |||||
 Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240
 Db |||||
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
 Db |||||
 Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300
 Db |||||
 Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIISDVPF 360
 Db |||||
 Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIISDVPF 360
 Db |||||
 Qy 361 KQTSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPTTHKPPPLYBERS 420
 Db |||||
 Qy 361 KQTSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPTTHKPPPLYBERS 420
 Db |||||
 Qy 421 PPLPKDLFQ 430
 Db |||||
 Qy 421 PPLPKDLFQ 430

RESULT 3

AAE23285
 ID AAE23285 standard; protein; 510 AA.

AC AAE23285;

DT 29-AUG-2003 (revised)

DT 27-AUG-2002 (first entry)

XX Mouse nectin-3-human nectin-3beta fusion protein.

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

OS Homo sapiens.

OS Mus musculus.

OS Chimeric.

XX Key Location/Qualifiers

XX Region 1..6

FT /note= "Mouse nectin-3 pprotein"

FT Region 7..510

FT /note= "Human nectin-3beta protein"

XX WO200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

DR N-ESDB; AAD37444.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.

XX

PS Claim 1; Page 94-95; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is a fusion protein encoding 6
 CC amino acids from mouse nectin-3 protein and the rest form human nectin-
 CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 510 AA;

Query Match 97.6%; Score 2243; DB 5; Length 510;

Best Local Similarity 99.5%; Pred. No. 8e-176;

Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLFSLRCGALAGPI 60

Db |||||

Qy 1 MARTRPSPLCPGGKAQLSSASLLGAGLLQLPPTPPPLLLFSLRCGALAGPI 60

Db |||||

Qy 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGFVQGEYQGR 120

Db |||||

Qy 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGFVQGEYQGR 120

Db |||||

Qy 121 VLFKNSLNDATITLHNIGSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Db |||||

Qy 121 VLFKNSLNDATITLHNIGSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Db |||||

Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240

Db |||||

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRGNLKNADANPPPF 300

Db |||||

Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIISDVPF 360

Db |||||

Qy 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIISDVPF 360

Db |||||

Qy 361 KQTSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPTTHKPPPLYBERS 420

Db |||||

Qy 361 KQTSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPTTHKPPPLYBERS 420

Db |||||

Qy 421 PPLPKDLFQ 430

Db |||||

Qy 421 PPLPKDLFQ 430

Db |||||

RESULT 4

AAE23284

ID AAE23284 standard; protein; 504 AA.

XX

AC AAE23284;

XX 27-AUG-2002 (first entry)

XX Human deleted nectin-3beta protein.

DE

XX

KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX Homo sapiens.
XX WO200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37443.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX Claim 1; Page 89-91; 14lpp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,
XX proliferation or angiogenic condition of a tissue or a subject, such as
XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX stroke, restenosis, tumour growth and treating herpesvirus infection.
XX Nectin is also useful for modulating proliferation or migration of an
XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
XX smooth muscle cell). The present sequence is human nectin-3beta protein
XX containing 6 amino acids deleted from the N-terminal end. Human nectin-
XX 3beta gene is located on chromosome 3
XX Sequence 504 AA;
Query Match 97.0%; Score 2229; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PSLPCPGGKAQSSASLLGAGLLQLPPTPPPLLLFPILLFSLRCLGALAGPIIPEVPHV 66
DB 1 PSLPCPGGKAQSSASLLGAGLLQLPPTPPPLLLFPILLFSLRCLGALAGPIIPEVPHV 60
QY 67 TAVGKGVSLKCLIEVNETITQISWEKHGKSSQTVAHVHPQYGFSGVQYGRVLFKNY 126
DB 61 TAVGKGVSLKCLIEVNETITQISWEKHGKSSQTVAHVHPQYGFSGVQYGRVLFKNY 120
QY 127 SLNDATITLNIIGFSDSGKVIKAVTFFPLGNAQSSSTTVTLVPTVSLIKGPSLIDGNN 186
DB 121 SLNDATITLNIIGFSDSGKVIKAVTFFPLGNAQSSSTTVTLVPTVSLIKGPSLIDGNN 180
QY 187 ETVAACIAATGKPVAHIDWEGDLEGEMESTTSPNETATIIISQYKLFPTFRFARGRITC 246
DB 181 ETVAACIAATGKPVAHIDWEGDLEGEMESTTSPNETATIIISQYKLFPTFRFARGRITC 240

QY 247 VVKHFALEKDIRYSFLIDIQAPESVGTGDNWFGVGRKGVNLKCNADANPPFPKSWSR 306
DB 241 VVKHFALEKDIRYSFLIDIQAPESVGTGDNWFGVGRKGVNLKCNADANPPFPKSWSR 300
QY 307 LDGQWPDGLASDNTLHFVHPTFTFNYGVYICKVTNSLQGRSDQKVIYISDVFPKQTSSI 366
DB 301 LDGQWPDGLASDNTLHFVHPTFTFNYGVYICKVTNSLQGRSDQKVIYISDVFPKQTSSI 360
QY 367 AVAGAVIGAVLALFIITAIFFVTLLTPRKRPSVLDKVIDLPPTHKPPPLYEERSPPLPQK 426
DB 361 AVAGAVIGAVLALFIITAIFFVTLLTPRKRPSVLDKVIDLPPTHKPPPLYEERSPPLPQK 420
QY 427 DLFQ 430
DB 421 DLFQ 424
RESULT 5
AAG63983
ID AAG63983 standard; protein; 510 AA.
XX AAG63983;
XX 26-NOV-2001 (first entry)
XX DT DT
XX DE Amino acid sequence of murine nectin-3.
XX KW Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
XX OS Mus sp.
XX PN WO200166736-A1.
XX PD 13-SEP-2001.
XX PF 09-MAR-2001; 2001WO-JP001871.
XX PR 09-MAR-2000; 2000JP-00065595.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PA (TAKA/) TAKAHASHI K.
XX PI Takahashi K, Takai Y, Nakanishi H, Sato K;
XX WPI; 2001-570771/64.
XX DR N-PSDB; AAH78180.
XX PT New protein family for diagnosing and treating tumor infiltration and
XX PT metastasis comprises the mouse nectin-3 protein families and
XX PT corresponding antibodies.
XX PS Claim 2; Page 45-48; 64pp; Japanese.
XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3
XX is an immunoglobulin-like cell adhesion molecule that shows homophilic
XX and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
XX polynucleotides are useful for investigating the mechanisms of cell
XX adhesion, infiltration and metastasis of cancer cells, the diagnosis of
XX malignancies of various cancers, and the development of methods for the
XX treatment and prevention of cancer
XX Sequence 510 AA;
Query Match 91.7%; Score 2108; DB 4; Length 510;
Best Local Similarity 92.2%; Pred. No. 1.1e-164;
Matches 400; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
QY 1 MARTLPSPLCPGCGKAQSSASLLGAGLLQLPPTPPPLLLFPILLFSLRCLGALAGPI 60
DB 1 MARTPGAPLCPGCGKAQSSAPPPRAGLLLPAPTPPPLLLLPILLFSLRCLGALAGSI 60
QY 61 IVPFHYTAVMGKGVSLKCLIEVNETITQISWEKHGKSSQTVAHVHPQYGFSGVQYGR 120
|||||

Db 61 IVEPHVTAVWGKNSVSKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGSFVQGDYQGR 120
 Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 Qy 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240
 Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240
 Qy 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
 Db 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
 Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
 Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
 Qy 361 KQTSIIAVAGAVIGAVLALFIITVFTVLLTPRKRPSYLDKVIDLPPTHKPPPLYERS 420
 Db 361 TQTSIIAVAGAVIGAVLALFIITVFTVLLTPRKRPSYLDKVIDLPPTHKPPPLYERS 420
 Qy 421 PPLPQKDLFQVCVH 434
 Db 421 PSLPQKDLGQTEH 434

RESULT 6
 AAEE23292
 ID AAE23292 standard; protein; 510 AA.
 AC AAEE23292;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Mouse nectin-3beta protein.
 XX
 KW Mouse; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma.
 XX
 OS Mus musculus.
 XX
 PN WO200228902-A2.
 XX
 PD 11-APR-2002.
 XX
 XX 05-OCT-2001; 2001WO-US031392.
 XX
 PR 05-OCT-2000; 2000US-0238557P.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 XX
 XX WPI; 2002-426103/45.
 XX
 DR Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 XX useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX
 XX Disclosure; Page 109-110; 141pp; English.
 XX
 PS The invention relates to a substantially purified nectin3alpha, beta,
 CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above

CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is mouse nectin-3beta protein
 XX
 SQ Sequence 510 AA;

Query Match 91.7%; Score 2108; DB 5; Length 510;
 Best Local Similarity 92.2%; Pred. No. 1.1e-164;
 Matches 400; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MARTLRSPICPGGKKAQLSSASLGGALLQPTPLALLLFPALLFRLCCALAGPI 60
 Db 1 MARTPGAPICPGGKKAQLSSAFPPAAGLLLPAPTPPPLLLLLLPALLFRLCCALAGSI 60
 Qy 61 IVEPHVTAVWGKNSVSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSFVQGEYQGR 120
 Db 61 IVEPHVTAVWGKNSVSKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGSFVQGDYQGR 120
 Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 Qy 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240
 Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPTRPAR 240
 Qy 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
 Db 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
 Qy 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
 Db 301 KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
 Qy 361 KQTSIIAVAGAVIGAVLALFIITVFTVLLTPRKRPSYLDKVIDLPPTHKPPPLYERS 420
 Db 361 TQTSIIAVAGAVIGAVLALFIITVFTVLLTPRKRPSYLDKVIDLPPTHKPPPLYERS 420
 Qy 421 PPLPQKDLFQVCVH 434
 Db 421 PSLPQKDLGQTEH 434

RESULT 7
 AAG63984
 ID AAG63984 standard; protein; 438 AA.
 XX
 AC AAG63984;
 XX

DT 26-NOV-2001 (first entry)

DE Amino acid sequence of murine nectin-3.

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

XX Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

PR 09-MAR-2000; 2000JP-00065595.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA (TAKA/) TAKAHASHI K.
 XX Takahashi K, Takai Y, Nakanishi H, Sato K;
 XX WPI; 2001-570771/64.
 DR N-PSDB; AAH78181.
 XX New protein family for diagnosing and treating tumor infiltration and
 PT metastasis comprises the mouse nectin-3 protein families and
 PT corresponding antibodies.
 XX Claim 3; Page 53-55; 64pp; Japanese.
 XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3
 CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
 CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
 CC polynucleotides are useful for investigating the mechanisms of cell
 CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
 CC malignancies of various cancers, and the development of methods for the
 CC treatment and prevention of cancer
 XX Sequence 438 AA;
 SQ
 Query Match 91.6%; Score 2107; DB 4; Length 438;
 Best Local Similarity 93.2%; Pred. No. 1e-164;
 Matches 399; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MARTLRPSPLCPGGGKAQLSSALLGAGLLLOPPTPPPLLLLPPLLLFRLCGALAGPI 60
 DB 1 MARTPGAPALCPGGGKAQLSSAPPAAGLLLPAPTTPPPLLLLPPLLLFRLCGALAGSI 60
 QY 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKHGKSQTVAHHHPQYGFSGVQYQGR 120
 DB 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKHGKSQTVAHHHPQYGFSGVQYQGR 120
 QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIQYKLPFTRFAR 240
 DB 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIQYKLPFTRFAR 240
 QY 241 GRITCVCVHPALEKDIRYFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
 DB 241 GRITCVCVHPALEKDIRYFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
 QY 301 KSVSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGQSDOKVIYISDVPF 360
 DB 301 KSVSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGQSDOKVIYISDVPF 360
 QY 361 KQTSIAVAGAVIGAVLALFTIAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLXYBERS 420
 DB 361 KQTSIAVAGAVIGAVLALFTIAIFVTVLLTPRKRPSTYLDKVIDLPPTHKPPPLXYBERS 420
 QY 421 PPLPQKDL 428
 DB 421 PSLPQKDL 428
 RESULT 8
 AAEE23293
 ID AAEE23293 standard; protein; 438 AA.
 XX AC AAEE23293;
 XX 27-AUG-2002 (first entry)
 XX Mouse nectin-3gamma protein.
 DE Mouse, nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
 KW paracellular transport disorder; kidney; allergy; diabetic retinopathy; allergy;
 KW

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
 KW stroke; tumour; cancer; herpesvirus infection; asthma.
 XX Mus musculus.
 OS WO200228902-A2.
 PN 11-APR-2002.
 PD 05-OCT-2001; 2001WO-US031392.
 XX 05-OCT-2000; 2000US-0238557P.
 PR (IMMV) IMMUNEX CORP.
 PA Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 PI WPI; 2002-426103/45.
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 PT useful for treating or preventing heart failure, malaria,
 PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
 PT sepsis, stroke.
 XX Disclosure; Page 111-112; 141pp; English.
 PS The invention relates to a substantially purified nectin3alpha, beta,
 CC nectin and nectin-4 polypeptides and their corresponding polynucleotides.
 CC Nectin DNA and protein are useful for treating a disease associated with
 CC cell adhesion activity, adherens junction formation activity, epithelial
 CC or endothelial barrier function activity, endothelial proliferation or
 CC migration activity, viral polypeptide binding activity. The epithelial or
 CC endothelial barrier function disorder which is treated by the above
 CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 CC asthma, allergy, allograft rejection, metastasis of cancer cells,
 CC paracellular transport disorders such as magnesium transport defects in
 CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 CC inhibiting angiogenesis in a mammal and treating endothelial migration,
 CC proliferation or angiogenic condition of a tissue or a subject, such as
 CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 CC stroke, restenosis, tumour growth and treating herpesvirus infection.
 CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is mouse nectin-3gamma protein
 XX Sequence 438 AA;
 SQ
 Query Match 91.6%; Score 2107; DB 5; Length 438;
 Best Local Similarity 93.2%; Pred. No. 1e-164;
 Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MARTLRPSPLCPGGGKAQLSSALLGAGLLLOPPTPPPLLLLPPLLLFRLCGALAGPI 60
 DB 1 MARTPGAPALCPGGGKAQLSSAPPAAGLLLPAPTTPPPLLLLPPLLLFRLCGALAGSI 60
 QY 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKHGKSQTVAHHHPQYGFSGVQYQGR 120
 DB 61 IVEPHVTAVGKNVSKCLIEVNETITQISWEKHGKSQTVAHHHPQYGFSGVQYQGR 120
 QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIQYKLPFTRFAR 240
 DB 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIQYKLPFTRFAR 240
 QY 241 GRITCVCVHPALEKDIRYFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
 DB 241 GRITCVCVHPALEKDIRYFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
 QY 301 KSVSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSIGQSDOKVIYISDVPF 360

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Db 301 KSWSRLDGQWPDGLLASDNTLHFVHPLTNYSVYVCKVNSLQSRDQKVIYISDIPL 360
Qy 361 KQTSSIAVAGAVIGAVIALFIITVLLTPPKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TQTSSIAVAGAVIGAVIALFIITVLLTPPKRPSYLDKVIDLPPTHKPPPLYEERI 420
Qy 421 PPLPQKDL 428
Db 421 PSUPQKDL 428

RESULT 9
AAE23290
ID AAE23290 standard; protein; 387 AA.
AC AAE23290;
XX
DT 27-AUG-2002 (first entry)
DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; aschma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..365
FT /note= "Human nectin-3alpha protein"
FT Region 366..381
FT /note= "FLAG peptide"
FT Region 382..387
FT /note= "PolyHis tag"
XX
XX WO200228902-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX PT useful for treating or preventing heart failure, malaria,
XX PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX PT sepsis, stroke.
XX
XX Claim 9; Page 105-107; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,

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CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta-
CC FLAGpolyHis fusion protein
XX
XX Sequence 387 AA;
SQ

Query Match      83.2%; Score 1912; DB 5; Length 387;
Best Local Similarity 99.5%; Pred. No. 1e-148;
Matches 363; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLOPPPPPLLLLLLFPILLFSLRCGALAGPI 60
Db 1 MARTPGSPPLCPGGGKAQLSSASLLGAGLLLOPPPPPLLLLLLFPILLFSLRCGALAGPI 60
Qy 61 IVEPHVTAVWGKVNLSKCLLEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSVOGEYQGR 120
Db 61 IVEPHVTAVWGKVNLSKCLLEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSVOGEYQGR 120
Qy 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTTPPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNATATIIISQKLPPTFRAR 240
Db 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNATATIIISQKLPPTFRAR 240
Qy 241 GRITCVVHKPALEKDIRYSFILDIOYAPEVSVTVGYDGNWVFGKGNLKNADANPPFP 300
Db 241 GRITCVVHKPALEKDIRYSFILDIOYAPEVSVTVGYDGNWVFGKGNLKNADANPPFP 300
Qy 301 KSWSRLDGQWPDGLLASDNTLHFVHPLTNYSVYICKVTNSLQSRDQKVIYISDVPP 360
Db 301 KSWSRLDGQWPDGLLASDNTLHFVHPLTNYSVYICKVTNSLQSRDQKVIYISDVPP 360
Qy 361 KQTSS 365
Db 361 KQTSS 365

RESULT 10
AAE23288
ID AAE23288 standard; protein; 595 AA.
AC AAE23288;
XX
XX 27-AUG-2002 (first entry)
XX Human nectin-3beta-IgGIFc region fusion protein.
XX
XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
XX paracellular transport disorder; kidney; diabetic retinopathy; allergy;
XX allograft rejection; metastasis; restenosis; inflammatory bowel disease;
XX oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
XX stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
XX cancer; asthma.
XX
XX Homo sapiens.
XX Unidentified.
XX Chimeric.
XX
XX WO200228902-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV ) IMMUNEX CORP.
XX

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CC Nectin is also useful for modulating proliferation or migration of an
 CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
 CC Human nectin-3alpha gene is located on chromosome 3
 XX
 SQ Sequence 549 AA;
 Query Match 82.8%; Score 1902.5; DB 5; Length 549;
 Best Local Similarity 79.3%; Pred. No. 9.7e-148;
 Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;
 QY 1 MARTLRSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLPFLFRLCGALAGPI 60
 DB 1 MARTLRSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLPFLFRLCGALAGPI 60
 QY 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGSVQYQGR 120
 DB 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGSVQYQGR 120
 QY 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFPAR 240
 DB 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFPAR 240
 QY 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTYGDNWFGVGRKGNLKNADANPPFP 300
 DB 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTYGDNWFGVGRKGNLKNADANPPFP 300
 QY 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP- 359
 DB 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDPT 360
 QY 360 -----FKQTSSIAVAGAVICAVLALFIIA 383
 DB 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLTATIKDDTIATIIASVVGALFIVLVS 420
 QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430
 DB 421 VLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES-----QIDVLQ 459
 RESULT 12
 ABJ20222
 ID ABJ20222 standard; protein; 549 AA.
 AC ABJ20222;
 XX
 DT 13-AUG-2003 (first entry)
 DE Human IG gene related protein SEQ ID No 45.
 XX Breast cancer; p53 pathway modulating agent; IG; colon cancer;
 KW kidney cancer; lung cancer; ovary cancer; human.
 XX Homo sapiens.
 OS
 XX WO200299040-A2.
 XX
 XX 12-DEC-2002.
 XX
 XX 03-JUN-2002; 2002WO-US017313.
 XX
 XX 05-JUN-2001; 2001US-0296076P.
 XX 10-OCT-2001; 2001US-0328605P.
 XX 22-OCT-2001; 2001US-0338733P.
 XX 15-FEB-2002; 2002US-0357253P.
 XX 15-FEB-2002; 2002US-0357600P.
 XX
 XX (EXEL-) EXELIXIS INC.
 XX

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI Lioubin MN;
 DR WPI; 2003-148660/14.
 XX
 PT Identifying a candidate p53 pathway modulators that are useful as targets
 PT for therapeutics or for diagnosing cancers associated with defective p53
 PT function, by providing an assay system having a purified IG polypeptide
 PT or nucleic acid.
 XX
 PS Claim 13; Page 206-209; 248pp; English.
 CC The invention relates to a novel method for identifying a candidate p53
 CC pathway modulating agent. The method comprises providing an assay system
 CC having a purified IG polypeptide or nucleic acid, or their functionally
 CC active fragment or derivative. The method is useful for identifying
 CC modulators of the p53 pathway, particularly for identifying agents for
 CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
 CC cancer or cancer of the ovary) associated with defective p53 function.
 CC The identified modulators are useful as targets for novel therapeutics.
 CC The method is also useful for diagnosing disorders associated with
 CC defective p53 function. The IG proteins or nucleic acids are useful as
 CC modifiers of the p53 pathway, and as therapeutic targets for disorders
 CC associated with defective p53 function. This sequence represents a human
 CC protein relating to the human IG genes used in the assay for identifying
 CC modulators of the p53 pathway of the invention
 XX
 SQ Sequence 549 AA;
 Query Match 82.8%; Score 1902.5; DB 6; Length 549;
 Best Local Similarity 79.3%; Pred. No. 9.7e-148;
 Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;
 QY 1 MARTLRSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLPFLFRLCGALAGPI 60
 DB 1 MARTLRSPICPGGKQAQLSSASLLGAGLLLOPPTPPPLLLPFLFRLCGALAGPI 60
 QY 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGSVQYQGR 120
 DB 61 IVEPHVTAVGKNSVLSKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGSVQYQGR 120
 QY 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 DB 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVEPTVSLIKGPD 180
 QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFPAR 240
 DB 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPPTFPAR 240
 QY 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTYGDNWFGVGRKGNLKNADANPPFP 300
 DB 241 GRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTYGDNWFGVGRKGNLKNADANPPFP 300
 QY 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP- 359
 DB 301 KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDPT 360
 QY 360 -----FKQTSSIAVAGAVICAVLALFIIA 383
 DB 361 TTTLOPTIQWHPSTADIEDLATEPKLPFPPLSTLTATIKDDTIATIIASVVGALFIVLVS 420
 QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 430
 DB 421 VLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES-----QIDVLQ 459
 RESULT 13
 ADR66369
 ID ADR66369 standard; protein; 549 AA.
 XX
 AC ADR66369;
 XX
 DT 02-DEC-2004 (first entry)

| | | | | | | |
|----|----|---|-----------|----------|---|-----|
| XX | DE | Human prostatic carcinoma derived protein SEQ ID 223 #2. | Db | 1 | MARTLRPSPLCGGKAQLSSASLLGALLQPPPTPPPLLLLPFLLLFSLRCLGALAGPI | 60 |
| XX | KW | human; cytostatic; diagnosis; prostatic cancer; differential expression analysis. | Qy | 61 | IVEPHVTAVWGKNSVLKCLIEVNETTQISWEKIHGKSSQTVAVHHPOYGFSGVQGEYQGR | 120 |
| XX | KW | | Db | 61 | IVEPHVTAVWGKNSVLKCLIEVNETTQISWEKIHGKSSQTVAVHHPOYGFSGVQGEYQGR | 120 |
| XX | OS | Homo sapiens. | Qy | 121 | VLFKNSLNDATTTLHNIQFSDSGKYICKAVTFPLGNAOSSTTVTLVEPTVSLIKGPD | 180 |
| XX | PN | WO2004076614-A2. | Db | 121 | VLFKNSLNDATTTLHNIQFSDSGKYICKAVTFPLGNAOSSTTVTLVEPTVSLIKGPD | 180 |
| XX | PD | 10-SEP-2004. | Qy | 181 | LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRPAR | 240 |
| XX | PF | 22-FEB-2004; 2004WO-DE000433. | Db | 181 | LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRPAR | 240 |
| XX | PR | 27-FEB-2003; 2003DE-01009985. | Qy | 241 | GRRITCVVHPALEKDIRSFILDIQYAPEVSVTGDGNWFWGKGNLKNADANPPPF | 300 |
| XX | PR | 14-MAY-2003; 2003DE-01022134. | Db | 241 | GRRITCVVHPALEKDIRSFILDIQYAPEVSVTGDGNWFWGKGNLKNADANPPPF | 300 |
| XX | PA | (HINZ/) HINZMANN B. | Qy | 301 | KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGORSDDKVIYISDVP | 359 |
| XX | PA | (DAHL/) DAHL E. | Db | 301 | KSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGORSDDKVIYISDVP | 359 |
| XX | PA | (ROSE/) ROSENTHAL A. | Qy | 360 | -----FKQTSIAVAGAVIGAVLALFIIA | 383 |
| XX | PA | (HERM/) HERMANN K. | Db | 361 | TTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFVLVS | 420 |
| XX | PA | (PILA/) PILARSKY C. | Qy | 384 | IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPLPKQDLFQ | 430 |
| XX | PI | Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T; Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S; Xinzhang L, Staub E; | Db | 421 | VLAGIFCYRRRTFRGDYFAK-----NYTPPSDMQKES-----QIDVLQ | 459 |
| XX | PI | WPI; 2004-653386/63. | RESULT 14 | | | |
| XX | PR | New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding agents. | ID | ADR66711 | standard; protein; 549 AA. | |
| XX | PS | Claim 2; Page 703; 1607pp; German. | XX | AC | ADR66711; | |
| XX | SS | This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention. | XX | DE | 02-DEC-2004 (first entry) | |
| XX | SS | Sequence 549 AA; | XX | DE | Human prostatic carcinoma derived protein SEQ ID 223 #3. | |
| XX | SQ | Query Match 82.8%; Score 1902.5; DB 8; Length 549; Best Local Similarity 79.3%; Pred. No. 9.7e-148; Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4; | XX | KW | human; cytostatic; diagnosis; prostatic cancer; differential expression analysis. | |
| XX | | | XX | KW | Homo sapiens. | |
| XX | | | XX | OS | WO2004076614-A2. | |
| XX | | | XX | PN | 10-SEP-2004. | |
| XX | | | XX | PF | 22-FEB-2004; 2004WO-DE000433. | |
| XX | | | XX | PR | 27-FEB-2003; 2003DE-01009985. | |
| XX | | | XX | PR | 14-MAY-2003; 2003DE-01022134. | |
| XX | | | XX | PA | (HINZ/) HINZMANN B. | |
| XX | | | XX | PA | (DAHL/) DAHL E. | |
| XX | | | XX | PA | (ROSE/) ROSENTHAL A. | |
| XX | | | XX | PA | (HERM/) HERMANN K. | |
| XX | | | XX | PA | (PILA/) PILARSKY C. | |
| XX | | | XX | PI | Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T; Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S; Xinzhang L, Staub E; | |
| XX | | | XX | PI | WPI; 2004-653386/63. | |
| XX | | | XX | PR | New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding agents. | |
| XX | | | XX | PS | Claim 2; Page 703; 1607pp; German. | |
| XX | | | XX | SS | This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention. | |
| XX | | | XX | SQ | Sequence 549 AA; | |
| XX | | | XX | | Query Match 82.8%; Score 1902.5; DB 8; Length 549; Best Local Similarity 79.3%; Pred. No. 9.7e-148; Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4; | |
| XX | | | XX | | 1 MARTLRPSPLCGGKAQLSSASLLGALLQPPPTPPPLLLLPFLLLFSLRCLGALAGPI | 60 |

XX This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.

XX SQ Sequence 549 AA;

Query Match 82.8%; Score 1902.5; DB 8; Length 549;

Best Local Similarity 79.3%; Pred. No. 9.7e-148; Indels 49; Gaps 4;

Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

Qy 1 MARTLRSPICPGGKQALSSASLLGALLLQPTPTPLLLLLFRLCGALAGPI 60
 Db 1 MARTLRSPICPGGKQALSSASLLGALLLQPTPTPLLLLLFRLCGALAGPI 60
 Qy 61 IVEPHVTAVMGKNSKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGSVQGYQGR 120
 Db 61 IVEPHVTAVMGKNSKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGSVQGYQGR 120
 Qy 121 VLFKNSLNDATITLHNIGSDSKYICKAVTFFLGNASQSTTTVTLVEPTVSLIKGPD 180
 Db 121 VLFKNSLNDATITLHNIGSDSKYICKAVTFFLGNASQSTTTVTLVEPTVSLIKGPD 180
 Qy 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTFRAR 240
 Db 181 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTFRAR 240
 Qy 241 GRRITCVVHPALEKDIRYSFILDIAVEPSVTVGDNWFGVRKGNLKNADANPPPF 300
 Db 241 GRRITCVVHPALEKDIRYSFILDIAVEPSVTVGDNWFGVRKGNLKNADANPPPF 300
 Qy 301 KSVWSRLDQWPDGLASDNTLHFVHLTFNYSYGVYICKVTNSLQGRSDQKVIYISDPV- 359
 Db 301 KSVWSRLDQWPDGLASDNTLHFVHLTFNYSYGVYICKVTNSLQGRSDQKVIYISDPPT 360
 Qy 360 -----PKQTSSIAVAGAVICAVIALFIIA 383
 Db 361 TTTTOPTIOWHPSTADIEDLATEPKLPFPPLUSTLATIKDDTIIAIVSGGALFIVLVS 420
 Qy 384 IFVTVLTLTPRK--RPSYLDKVIDLPPHTKPPPLYEERSPPLPKQDLFP 430
 Db 421 VLAGIFCYRRRTTRGDYFAK-----NYIPSDMQKES-----QIDVLQ 459

RESULT 15
 AAE23282

ID AAE23282 standard; protein; 549 AA.
 AC AAE23282;
 XX 29-AUG-2003 (revised)
 DT 27-AUG-2002 (first entry)
 XX Mouse nectin-3-human nectin 3alpha fusion protein.
 DE Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
 XX paracellular transport disorder; kidney; diabetic retinopathy; allergy;
 KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
 KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
 KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
 XX chromosome 3.
 OS Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT Region 1..7
 FT /note= "Mouse nectin-3 protein"
 FT Region 8..549
 FT /note= "Human nectin-3alpha protein"
 FT WO200228902-A2.
 XX 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US031392.
 XX 05-OCT-2000; 2000US-0238557P.
 XX (IMMV) IMMUNEX CORP.
 XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
 XX WPI; 2002-426103/45.
 XX N-PSDB; AAD37441.
 XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
 XX useful for treating or preventing heart failure, malaria,
 XX glomerulonephritis, endometriosis, leukemia, allergy, edema,
 XX sepsis, stroke.
 XX Claim 1; Page 80-82; 141pp; English.
 XX The invention relates to a substantially purified nectin3alpha, beta,
 XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
 XX Nectin DNA and protein are useful for treating a disease associated with
 XX cell adhesion activity, adherens junction formation activity, epithelial
 XX or endothelial barrier function activity, endothelial proliferation or
 XX migration activity, viral polypeptide binding activity. The epithelial or
 XX endothelial barrier function disorder which is treated by the above
 XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
 XX asthma, allergy, allograft rejection, metastasis of cancer cells,
 XX paracellular transport disorders such as magnesium transport defects in
 XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
 XX inhibiting angiogenesis in a mammal and treating endothelial migration,
 XX proliferation or angiogenic condition of a tissue or a subject, such as
 XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
 XX stroke, restenosis, tumour growth and treating herpesvirus infection.
 XX Nectin is also useful for modulating proliferation or migration of an
 XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
 XX smooth muscle cell). The present sequence is a fusion protein containing
 XX mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
 XX alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
 XX standardise OS field)
 XX Sequence 549 AA;

Query Match 82.1%; Score 1888.5; DB 5; Length 549;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2005, 09:42:42 ; Search time 14.3671 Seconds
(without alignments)
2926.593 Million cell updates/sec

Title: US-09-972-268-31
Perfect score: 2299
Sequence: 1 MANTLRPSPLCPGGKRAQLS.....ERSPPLPKDQLFQVCVHEYT 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 1159.5 | 50.4 | 407 | 2 T08732 | hypothetical prote |
| 2 | 544 | 23.7 | 518 | 2 JC4024 | poliovirus recepto |
| 3 | 495.5 | 21.6 | 530 | 2 A53437 | PRR2 delta - human |
| 4 | 490 | 21.3 | 538 | 2 T68093 | poliovirus recepto |
| 5 | 467 | 20.3 | 467 | 1 HLMSF3 | PRR2 alpha - human |
| 6 | 455 | 19.8 | 478 | 2 I53960 | poliovirus recepto |
| 7 | 418 | 18.2 | 392 | 2 B44194 | poliovirus recepto |
| 8 | 418 | 18.2 | 417 | 2 A44194 | poliovirus recepto |
| 9 | 402 | 17.5 | 392 | 1 RWHUPD | poliovirus recepto |
| 10 | 326.5 | 14.2 | 416 | 2 A54017 | poliovirus recepto |
| 11 | 326.5 | 14.2 | 416 | 2 A54017 | poliovirus recepto |
| 12 | 229.5 | 10.0 | 764 | 2 A49448 | irregular chiasm C |
| 13 | 205.5 | 8.9 | 4391 | 2 A38096 | perlecan precursor |
| 14 | 196.5 | 8.5 | 5175 | 2 T20992 | hypothetical prote |
| 15 | 196.5 | 8.5 | 5198 | 2 T43290 | hemectin precurs |
| 16 | 187.5 | 8.2 | 274 | 2 A47639 | OX-2 membrane glyco |
| 17 | 178 | 7.7 | 588 | 2 JH0506 | adhesion molecule |
| 18 | 178 | 7.7 | 588 | 2 A45254 | surface glycoprote |
| 19 | 177.5 | 7.7 | 853 | 1 IJBONC | neural cell adhesi |
| 20 | 177 | 7.7 | 626 | 1 A61084 | myelin-associated |
| 21 | 177 | 7.7 | 637 | 2 B33785 | myelin-associated |
| 22 | 176 | 7.7 | 7962 | 2 I38346 | elastic titin - hu |
| 23 | 175 | 7.6 | 582 | 1 ENRT3S | myelin-associated |
| 24 | 175 | 7.6 | 626 | 1 ENRT3S | myelin-associated |
| 25 | 174.5 | 7.6 | 1896 | 2 T08851 | Down syndrome cell |
| 26 | 173.5 | 7.5 | 3707 | 2 S18252 | heparan sulfate pr |
| 27 | 171 | 7.4 | 1091 | 2 A58532 | glial cell membran |
| 28 | 170.5 | 7.4 | 365 | 2 JC780 | coxsackie- and ade |
| 29 | 164.5 | 7.2 | 847 | 2 JH0371 | B-cell adhesion pr |

| | | | | | |
|----|-------|-----|------|----------|---------------------|
| 30 | 162.5 | 7.1 | 278 | 1 TDRTOX | OX-2 membrane glyco |
| 31 | 162.5 | 7.1 | 858 | 1 IJRTNC | neural cell adhesi |
| 32 | 162 | 7.0 | 587 | 2 JH0464 | DM-GRASP precursor |
| 33 | 162 | 7.0 | 761 | 1 IJHUNG | neural cell adhesi |
| 34 | 162 | 7.0 | 765 | 2 C42632 | cell adhesion mole |
| 35 | 162 | 7.0 | 812 | 2 B42632 | cell adhesion mole |
| 36 | 162 | 7.0 | 932 | 2 A42632 | cell adhesion mole |
| 37 | 160.5 | 7.0 | 702 | 2 A36319 | carcinoembryonic a |
| 38 | 157 | 6.8 | 739 | 1 JN0581 | vascular cell adhe |
| 39 | 157 | 6.8 | 1091 | 1 IJCHNL | neural cell adhesi |
| 40 | 156 | 6.8 | 646 | 2 I38049 | cell surface glyco |
| 41 | 154.5 | 6.7 | 509 | 2 JCS288 | SHIP substrate-1 pr |
| 42 | 154 | 6.7 | 1612 | 2 T30805 | duffy protein - mo |
| 43 | 153.5 | 6.7 | 723 | 1 IJMSNG | neural cell adhesi |
| 44 | 153.5 | 6.7 | 1115 | 1 IJMSNG | neural cell adhesi |
| 45 | 153 | 6.7 | 1051 | 2 A39712 | kinase-like protei |

ALIGNMENTS

RESULT 1

T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: UNIPROT:Q9Y412; EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 50.4%; Score 1159.5; DB 2; Length 407;
Best Local Similarity 70.3%; Pred. No. 1.1e-77;
Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

| | | | |
|----|-----|--|-----|
| Qy | 143 | SGYICKAVTFPLGNAQSSTTVLVEPTVSLIKGPDLSIDGGNETVAAICIAATGKPA | 202 |
| Db | 1 | SGYICKAVTFPLGNAQSSTTVLVEPTVSLIKGPDLSIDGGNETVAAICIAATGKPA | 60 |
| Qy | 203 | HIDWEGDLGEMESTTTSFPNETATIIISQYKLPTRFARGRRITCVVKHPALEKDIRYSFI | 262 |
| Db | 61 | HIDWEGDLGEMESTTTSFPNETATIIISQYKLPTRFARGRRITCVVKHPALEKDIRYSFI | 120 |
| Qy | 263 | LDIOYAPEVSVTCYDGNWFGVGRKGNLKNADANPPPKSVWSRLDQWPDGLASDNTL | 322 |
| Db | 121 | LDIOYAPEVSVTCYDGNWFGVGRKGNLKNADANPPPKSVWSRLDQWPDGLASDNTL | 180 |
| Qy | 323 | HFVHPLTFNYSGVYICKVNTSLGORSQDKYIYISDVP----- | 359 |
| Db | 181 | HFVHPLTFNYSGVYICKVNTSLGORSQDKYIYISDPTTTTLQPTIQWHFSTADIEDLAT | 240 |
| Qy | 360 | -----FKQTSIAVAGAVIGAVLAFIAFVTLVLLTPRK--RPSYLDKV | 403 |
| Db | 241 | EPKKLPPLTLATIKDDTIATIIISVVGGLFVLVSLAGIFCYVRRRTFRGDYPAK- | 299 |
| Qy | 404 | IDLPPTHKPPPLYEERSPPLPQKDLFQ | 430 |
| Db | 300 | -----NYIPSPDMQKES-----QIDVLQ | 317 |

RESULT 2

JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024

R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubh
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: JC4024; MUID:95237621; PMID:7721102
A;Accession: JC4024
A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C;Genetics:
A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: Glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status predicted <TM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.7%; Score 544; DB 2; Length 518;
Best Local Similarity 33.4%; Pred. No. 2.6e-32;
Matches 119; Conservative 68; Mismatches 129; Indels 40; Gaps 8;

Qy 71 GKNVSLKCLIE--VNETTIQISWEKTHGKSSQTAVVHHPOYGFSGVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNSMGVSLAPYRVERVEFLRPS 103

Qy 128 LNDATTILHNGSDSKYICKAVTFFPLGNAQSSTTVTLVLEPTVSLIKGPDLSLDG--- 184
Db 104 FTDGTLRLSRLEDEGVICEFATFPTGNRESQNLTVMAKPT-NWIEGTQVLAACKG 162

Qy 185 -GNETVAAICIAATGKVAHDWE-----GDLGEMESTTSPNETATIIISOYKL 233
Db 163 QDDKVLVATCTSANGKPPSVSWETRUKGEARVPDGSQT-----PMAPVTIVISRYRL 214

Qy 234 FPTRFARGRRITCVVHPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGVNLKCN 293
Db 215 VPSREAHQQLACIVNYHM--DRFKESLTNLVQYEPVETIEGFDGNWYLRMDVKLTCKA 272

Qy 294 DANPPPPKSVWSRLDQWPGDLASDNLHFVHPLTFNYSGVYICKVTNSLGRQSDOKVI 353
Db 273 DANPPATEYHWTTLINGSLPKGVEAQNRTLFPKGPINYSLAGTYCEATNPIGTRSGQVEV 332

Qy 354 YISDVPEPKQTS-----STAVAGAVIGAVIALFIIAIFVTVLLTPRKRPSPY 399
Db 333 NITEFPYTPSPPEHGRAGPVPTAIIIGVAGSILLVIVGGIVVAL--RRRRHTP 386

RESULT 3
A53437
Poliovirus receptor mpVR - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53437
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with P
A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
A;Cross-references: UNIPROT:P32507; GB:D26107; NID:g475017; PIDN:BA05103.1; PID:g825507
A;Experimental source: C57BL/6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBI:P:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>

Query Match 21.6%; Score 495.5; DB 2; Length 530;
Best Local Similarity 30.6%; Pred. No. 1e-28;
Matches 133; Conservative 72; Mismatches 188; Indels 41; Gaps 14;

Qy 30 LLQPPTPPPLLLLPDLLLSRLCGALAGPIIVEPHVTAVMGKNVSLKC--LIEVNETIT 87

Db 6 VLPPGRSLPTLLPLLLLLLOETGAQDVRVRVLPVGRGLGTVLPCHLLPPTTTERVS 65
Qy 88 QISWEKIHCKSSQTVAVVHHPOYGFSGVQGEY--QGRVLF-----KNYSLNDATITLHNIG 139
Db 66 QVTWORLDG---TVVAAFHPSFGVDFPNQSKDRLSFVRARPETWADLRDATLAFRGLR 122
Qy 140 FDSGKVIKCAVTFPFLGNAQSSTTVTLVLEP-----TVSLIKGPDLSLDGNETVAAICI 194
Db 123 VEDEGNYTCEFATFPNGTREGVTWLRVIAQENHAEQAQEVITGPQSV-----AVARCV 175
Qy 195 AATGKPVAHIDWEGDLGEMESTTTSPFN---ETATIIISOYKLPPTPARGRRITCVVKHP 251
Db 176 STGGRPPARITWISSLGG-EAKDTQBPQIAGTQAGTIIISRYSLVPVGRADGVKVTCTRVEHE 234
Qy 252 ALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGVNLKCNADANPPPKSVMSRLDGOW 311
Db 235 SFEETILLPVTLSVRYPPEVSIISGVDNWLGRSEAILTCDVRNSPEPTDYDWTSTSGVF 294

Qy 312 PDGLASDNLHFVHPLTFNYSGVYICKVTNSLGRQSDOKVIYISDVPEPKQTSIIAVAGA 371
Db 295 PASAVAQGSQQL-LVHSVDRMVNTTFCITATNAVGTGRAEQVILVRESP--STAGAGATGG 351

Qy 372 VIGAVLALFI-IAIFVTVLLTPRKRPSPYL-----DKVIDLPPTHKPP-PLYEERSPL 423
Db 352 IIGGIITAAIATAVAGTGILICRQKQKQRLQAADDEELEGPPSYKPPTPKAKLBEPEM 411

Qy 424 PQKDLFOVCVHEYT 437
Db 412 PSQ-LFTLGASEHS 424

RESULT 4
R68093
PRR2 delta - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I68093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I68093
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-538 <RES>
A;Cross-references: UNIPROT:Q92692; GB:S79172; NID:g1042204; PID:g1042205
C;Genetics:
A;Gene: PRR2delta
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 21.3%; Score 490; DB 2; Length 538;
Best Local Similarity 29.3%; Pred. No. 2.6e-28;
Matches 130; Conservative 79; Mismatches 174; Indels 60; Gaps 16;

Qy 33 PPTPPPLLLLPDLLLSRL-CGALAGPIIVEPHVTAVMGKNVSLKCLII---EWNETITQ 88
Db 13 PPTP-----LLWPLLLLLLETTGAQDVRVQVLPVGRQLGGTVLPCHLLPVPVGLYISL 67

Qy 89 ISWEKTHGKSS-QTVAVVHHPOYGFSGVQGEYQ--RVLF-----KNYSLNDATITL 135
Db 68 VTWQRDPAHQNVAAAFHPKMGPSFPKPSGERLSFSVSAKOSTGQDTEAEQLDATAL 127

Qy 136 HNTGFSDSGKYICKAVTFFPLGNAQSSTTVTLVLEP-----TVSLIKGPDLSLDGNET 188
Db 128 HGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPNQAEQAQVTFSDP-----T 178

Qy 189 VAAICIAATGKPVAAHI-----DWEGDLGEMESTTTISFPNETATIIISOYKLPPTRFARGR 242
Db 179 TVALCISKEGRPPPARISWLSLSDWEAKETQVSGTLAG----TIVTVTRFTLVFSGRADGV 234

Qy 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTYGDNWFGVGRKGVNLKCNADANPPPFKS 302

Query Match 8.5%; Score 196.5; DB 2; Length 5198;
Best Local Similarity 26.4%; Pred. No. 1.8e-05;
Matches 88; Conservative 42; Mismatches 138; Indels 65; Gaps 19;

```

Qy 59 PIIVE-PHVTAV-WGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGE 116
Db 793 PTIESPHTVRVNIERQVTIQLCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847
Qy 117 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAOSSTT--VTVLVEPTVSL 174
Db 848 -----NLLITDAQI-----EDQGFTCIARN-TYQQSQSSTTLMVTGLVSPVLGH 891
Qy 175 IKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLF 234
Db 892 VPPEEQIIEGQDITLS--CVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSL 943
Qy 235 PTRFARGR---RITCVVKKHPALEKDIRYSFIL----DIQYAPE-----VSVTGYDGNW- 280
Db 944 RLGGNPKDEGKYCTIAVSPAGNSTLHINVQLIKPEFVYKPEGGIVFKPTISGMDEKHV 1003
Qy 281 -----FVGRKGVNLKCNADANPPPKSVWSRLDQWP-----DGLLASDNTLHFVH 326
Db 1004 AVVNSTHDVLDGEGFAIPCVVSGTPPPI-ITW-YLDGR-EITPNSRDFVTADNTL-IVR 1059
Qy 327 PLTFNYSGVYICKVWNSLQORSQDKVIYISDVP 359
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTIIRIMNTP 1092

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Search completed: October 6, 2005, 10:21:12
Job time : 15.3671 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2005, 09:34:02 ; Search time 64.8231 Seconds
(without alignments)
3452.143 Million cell updates/sec

Title: US-09-972-268-31

Perfect score: 2299

Sequence: 1 MARTLRSPICPGGKQAQLS.....ERSPPLPKDLFQVCVHEYT 437

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 2108 | 91.7 | 510 | 2 Q9JLB8 | Q9JLB8 mus musculus |
| 2 | 2107 | 91.6 | 438 | 2 Q9JLB7 | Q9JLB7 mus musculus |
| 3 | 1902.5 | 82.8 | 549 | 2 Q9NQ33 | Q9NQ33 homo sapien |
| 4 | 1872 | 81.4 | 366 | 2 Q6NV23 | Q6NV23 homo sapien |
| 5 | 1803 | 78.4 | 549 | 2 Q9JLB9 | Q9JLB9 mus musculus |
| 6 | 1759 | 76.5 | 549 | 2 Q9D006 | Q9D006 mus musculus |
| 7 | 1235 | 53.7 | 267 | 2 Q9NC05 | Q9NC05 homo sapien |
| 8 | 1159.5 | 50.4 | 407 | 2 Q9Y412 | Q9Y412 homo sapien |
| 9 | 630.5 | 27.4 | 304 | 2 Q9EVA9 | Q9EVA9 homo sapien |
| 10 | 580 | 25.2 | 515 | 1 PVR1 MOUSE | Q9Jkf6 mus musculus |
| 11 | 575 | 25.0 | 515 | 1 PVR1 MOUSE | Q9Jkf6 mus musculus |
| 12 | 566.5 | 24.6 | 517 | 1 PVR1 HUMAN | Q9J223 homo sapien |
| 13 | 564.5 | 24.6 | 515 | 1 PVR1 PIG | Q9Jl76 sus scrofa |
| 14 | 534.5 | 23.2 | 295 | 2 Q9ERF5 | Q9ERF5 mesocricetu |
| 15 | 528 | 23.0 | 298 | 2 Q9GL74 | Q9GL74 cercopithec |
| 16 | 526.5 | 22.9 | 295 | 2 Q9GL75 | Q9GL75 bos taurus |
| 17 | 522 | 22.7 | 510 | 2 Q96NV8 | Q96NV8 homo sapien |
| 18 | 521 | 22.7 | 510 | 2 Q96K15 | Q96K15 homo sapien |
| 19 | 497.5 | 21.6 | 464 | 2 Q6GL25 | Q6GL25 xenopus tro |
| 20 | 495.5 | 21.6 | 530 | 1 PVR2 MOUSE | P32507 mus musculus |
| 21 | 495.5 | 21.6 | 530 | 2 Q80XJ5 | Q80XJ5 mus musculus |
| 22 | 494 | 21.5 | 483 | 2 Q9DBP8 | Q9DBP8 mus musculus |
| 23 | 494 | 21.5 | 508 | 2 Q9CED8 | Q9CED8 mus musculus |
| 24 | 494 | 21.5 | 508 | 2 Q9R007 | Q9R007 mus musculus |
| 25 | 490 | 21.3 | 538 | 1 PVR2 HUMAN | Q92692 homo sapien |
| 26 | 488 | 21.2 | 463 | 2 Q66J72 | Q66J72 xenopus lae |
| 27 | 467 | 20.3 | 467 | 2 Q8C6F2 | Q8C6F2 mus musculus |
| 28 | 467 | 20.3 | 467 | 2 Q91VT9 | Q91VT9 mus musculus |
| 29 | 427.5 | 18.6 | 449 | 2 Q9UE16 | Q9UE16 homo sapien |
| 30 | 418 | 18.2 | 417 | 1 PVR_CERAE | P32506 cercopithec |
| 31 | 411.5 | 17.9 | 412 | 2 Q9R1E1 | Q9R1E1 rattus norv |

| | | | | | |
|----|-------|------|-----|-------------|---------------------|
| 32 | 407 | 17.7 | 400 | 2 Q8HY16 | Q8HY16 cebus apell |
| 33 | 406.5 | 17.6 | 412 | 2 Q63611 | Q63611 rattus norv |
| 34 | 405 | 17.6 | 417 | 1 PVR_HUMAN | P15151 homo sapien |
| 35 | 402.5 | 17.5 | 408 | 2 Q91WP1 | Q91WP1 mus musculus |
| 36 | 400.5 | 17.4 | 408 | 2 Q8K094 | Q8K094 m hypotheri |
| 37 | 399.5 | 17.4 | 408 | 2 Q8BVF6 | Q8BVF6 mus musculus |
| 38 | 395 | 17.2 | 401 | 2 Q88835 | Q88835 cercopithec |
| 39 | 390 | 17.0 | 403 | 2 Q8HY15 | Q8HY15 lemur catta |
| 40 | 386 | 16.8 | 412 | 2 Q8HY14 | Q8HY14 oryctolagus |
| 41 | 355.5 | 15.5 | 415 | 2 Q6O977 | Q6O977 mus musculus |
| 42 | 326.5 | 14.2 | 416 | 2 Q7M048 | Q7M048 rattus norv |
| 43 | 309 | 13.4 | 417 | 2 Q7TNL1 | Q7TNL1 mus musculus |
| 44 | 305.5 | 13.3 | 442 | 2 Q9BY67 | Q9BY67 homo sapien |
| 45 | 304.5 | 13.2 | 390 | 2 Q66KX2 | Q66KX2 xenopus lae |

ALIGNMENTS

RESULT 1

Q9JLB8 PRELIMINARY; PRT; 510 AA.
AC Q9JLB8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 beta.
GN Name=Evr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195834; AAF63686.1; -
DR MGD; MGI:1930171; Evr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 510 AA; 55811 MW; 45CF66EF78454864 CRC64;

Query Match 91.7%; Score 2108; DB 2; Length 510;

Best Local Similarity 92.2%; Pred. No. 2.5e-155;

Matches 400; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MARTLRSPICPGGKQAQLSSALLGALLLQPTPPPLLLLFLLLSLCCALAGPI | 60 |
| Db | 1 | MARTPGAPLCPGGKQAQLSAPPAPPAAGLLLPAPTPPPLLLLFLLLSLCCALAGSI | 60 |
| Qy | 61 | IVEPHVTAVGKNSVKLCLEVNVTIQTISWEKHGKSSQTVAVHHQYGFSGVQGR | 120 |
| Db | 61 | IVEPHVTAVGKNSVKLCLEVNVTIQTISWEKHGKSTQTVAVHHQYGFSGVQGR | 120 |
| Qy | 121 | VLFPKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVPEVTSI | 180 |
| Db | 121 | VLFPKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSTTTVTLVPEVTSI | 180 |
| Qy | 181 | LIDGGNTVAACIAATGKPVAHIDWEGDLGEMSTTSPNETATISQYKLPFPAR | 240 |

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Db 181 LIDGNETVAACVAAATGKPVQAIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
QY 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDVPP 360
Db 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDIPL 360
QY 361 KOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPSPYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPSPYLDKVIDLPPTHKPPVVEERI 420
QY 421 PPLPOKDLFOVCVH 434
Db 421 PSLPQKDLIGQTEH 434

RESULT 2
Q9JULB7 PRELIMINARY; PRT; 438 AA.
AC Q9JULB7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN Name=Pvr13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PSS0835; IG LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

Query Match 91.6%; Score 2107; DB 2; Length 438;
Best Local Similarity 93.2%; Pred. No. 2.4e-155;
Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 MARTLPSPLCPGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPLLLFSRLCGALAGPI 60
Db 1 MARTPGAPLCPGGKAQLSSAPPAAGLLLPAPTPPPPLLLLIPLLLFSRLCGALAGSI 60
QY 61 IVEPHTVAVGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHHPQYGSVQGYQGR 120
Db 61 IVEPHTVAVGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHHPQYGSVQGYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVLVVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVLVVEPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
QY 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDVPP 360
Db 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDIPL 360
QY 361 KOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPSPYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPSPYLDKVIDLPPTHKPPVVEERI 420
QY 421 PPLPOKDLFOVCVH 434
Db 421 PSLPQKDLIGQTEH 434
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Db 181 LIDGNETVAACVAAATGKPVQAIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
QY 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDVPP 360
Db 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDIPL 360
QY 361 KOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPSPYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TOTSSIAVAGAVIGAVLALFIITVTVLLTPRKRPSPYLDKVIDLPPTHKPPVVEERI 420
QY 421 PPLPOKDL 428
Db 421 PSLPQKDL 428

RESULT 3
Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin."
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 82.8%; Score 1902.5; DB 2; Length 549;
Best Local Similarity 79.3%; Pred. No. 2.6e-139;
Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 1 MARTLPSPLCPGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPLLLFSRLCGALAGPI 60
Db 1 MARTLPSPLCPGGKAQLSSASLLGAGLLLOPPTPPPLLLLFPLLLFSRLCGALAGPI 60
QY 61 IVEPHTVAVGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHHPQYGSVQGYQGR 120
Db 61 IVEPHTVAVGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHHPQYGSVQGYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVLVVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSSTTVLVVEPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
Db 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFAR 240
QY 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
Db 241 GRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
QY 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDVPP 359
Db 301 KSWSRDLGQWPDGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISDPT 360
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Qy 360 -----FKQTSIAVAGAVICAVLAFIIA 383
Db 361 TTTLOPTQIHPSTADIEDLATEPKLPFPPLSLATIKODDTIATIIASVVGALFIVLS 420
Qy 384 IFVTVLLTPRKK--RPSVLDKVIDLPPPHKPPPLPEERSPPLPKDLFQ 430
Db 421 VLAGIFCYRRRTFRGDYFAK-----NYIPSDMQKES-----QIDVLQ 459

RESULT 4
Q6NVZ3
ID Q6NVZ3 PRELIMINARY; PRT; 366 AA.
AC Q6NVZ3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PVRL3 protein.
GN Name=PVRL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067808; AAH67808.1; -.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 3.
SQ SEQUENCE 366 AA; 39722 MW; 591D0A4687C630BA CRC64;

Query Match 81.4%; Score 1872; DB 2; Length 366;
Best Local Similarity 99.7%; Pred. No. 3.6e-137;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLIQPPTPPPLLLPFLLSLCLGALAGPI 60
Db 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLIQPPTPPPLLLPFLLSLCLGALAGPI 60

Qy 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120

Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

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Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTFR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTFR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGNLKNADANPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGNLKNADANPPF 300
Qy 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGQRSDQKVIYIS 356
Db 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGQRSDQKVIYIS 356

RESULT 5
Q9JLB9
ID Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN Name=PVRL3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716; DOI=10.1074/jbc.275.14.10291;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3, a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MG; MG1:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60582 MW; 5492C9ABB472F185 CRC64;

Query Match 78.4%; Score 1803; DB 2; Length 549;
Best Local Similarity 73.2%; Pred. No. 1.4e-131;
Matches 357; Conservative 26; Mismatches 47; Indels 58; Gaps 5;

Qy 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLIQPPTPPPLLLPFLLSLCLGALAGPI 60
Db 1 MARTLRPSPLCPGGKQAQLSSASLLGAGLLIQPPTPPPLLLPFLLSLCLGALAGPI 60

Qy 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Db 61 IVEPHVTAVMGKNSVLSKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120

Qy 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTFR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTFR 240
Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGNLKNADANPPF 300

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Db 241 GRITCVKHPALEKDIRYSFLLDIQYAPEVSVTGDNWFGVGRGNLKNADANPPPF 300
QY 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDOKVIYISDVPF 360
Db 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYCKVNSLQSGSDOKVIYISDPPT 360
QY 361 KQT-----SSIA-----VAGAVIGAVLALFIIA 383
Db 361 TTTLQPTVQWHSPPADVDIATEHKKLPPLSLTLATLKDDTIGTIIASVVGALFLVLS 420
QY 384 IFVTVLLTPRKR-----PSYLDKVIDLPPTHK-----PPPLYERSPP--- 422
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPFSDMQESQIDVLHQDELSDYPSVKENKPNVNN 480
QY 423 LPQKDLFQ 430
Db 481 LIRKDYLE 488

RESULT 6
Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610301B19 product:poliovirus receptor-related
DE 3, full insert sequence.
GN Names=Pvrl3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanaoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuura T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PPS0835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

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Query Match 76.5%; Score 1759; DB 2; Length 549;
Best Local Similarity 71.5%; Pred. No. 3.7e-128;
Matches 349; Conservative 29; Mismatches 58; Gaps 5;

QY 1 MARTLPSPCLCPGGKQAQLSSALLGALLLOPPTPPPLLLLPLLSRLCGALAGPI 60
Db 1 MARTCPAPCLCPGGKQAQLSSAFPAPGALLLPAPTTPPLLLLPLLSRLCGALAGSI 60
QY 61 IVEPHVTAVGKNVSLKCLIEVNETTQISWEKHOKSSQTVAHVHPQGFSGVQYQGR 120
Db 61 IVEPHVTAVGKNVSLKCLIEVNETTQISWEKHGKSTQTVAHVHPQGFSGVQYQGR 120
QY 121 VLFKNYSLNDATTTLHNIGFSDSGKYICKAVTPPLGNAQSSSTVTVLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTTLHNIGFSDSGKYICKAVTPPLGNAQSSSTVTVLVEPTVSLIKGPD 180
QY 181 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKLFPTFRFAR 240
Db 181 SIDGNETVAAVCVSGTGPVQIDWEGDLGEREFSTISFLNETATIVSQYELFPTFRFAR 240
QY 241 GRRITCVKHPALEKDIRYSFLLDIQYAPEVSVTGDNWFGVGRGNLKNADANPPPF 300
Db 241 GRRITCVKHPALEKDIRYSFLLDIQYAPEVSVTGDNWFGVGRGNLKNADANPPPF 300
QY 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSGSDOKVIYISDVPF 360
Db 301 KSVMSRLDQGWPDGLASDNTLHFVHPLTFNYSGVYCKVNSLQSGSDOKVIYISDPPT 360
QY 361 KQT-----SSIA-----VAGAVIGAVLALFIIA 383
Db 361 TTTLQPTVQWHSPPADVDIATEHKKLPPLSLTLATLKDDTIGTIIASVVGALFLVLS 420
QY 384 IFVTVLLTPRKR-----PSYLDKVIDLPPTHK-----PPPLYERSPP--- 422
Db 421 ILAGVFCYRRRTFRGDYFAKNYIPFSDMQESQIDVLHQDELSDYPSVKENKPNVNN 480

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QY 423 LPQKDLFQ 430
Db 481 LIRKDYLE 488

RESULT 7
Q8NC05 PRELIMINARY; PRT; 267 AA.
AC Q8NC05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masubo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PSS0835; IG-LIKE; 2.
KW Receptor.
SQ SEQUENCE 267 AA; 29253 MW; 4P464A8A1BA0C451 CRC64;

Query Match 53.7%; Score 1235; DB 2; Length 267;
Best Local Similarity 96.0%; Pred. No. 8.2e-86;
Matches 242; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 41 LLLPPL--LFSRLCGALAGPIIPEPHVAVWGNVSLKCLIEVNETITQISWEKINGKS 98
Db 16 LLRGLPLPRFSGNPRALAGPIIPEPHVAVWGNVSLKCLIEVNETITQISWEKINGKS 75

QY 99 SQTVAHHPOYGFVSQGEYQGRVLFNKNSLNDATITLHNGFSDSGKYICKAVTFPLGNA 158
Db 76 SQTVAHHPOYGFVSQGEYQGRVLFNKNSLNDATITLHNGFSDSGKYICKAVTFPLGNA 135

QY 159 QSSTTVTLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 218
Db 136 QSSTTVTLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTT 195

QY 219 SFPNETATIIISQYKLPFTRFARGRRITCVVKGHPALEKDIRYSFTLDIOYAPEVSVTYGD 278
Db 196 SFPNETATIIISQYKLPFTRFARGRRITCVVKGHPALEKDIRYSFTLDIOYAPEVSVTYGD 255

QY 279 NWFVGRKGVLNK 290
Db 256 NWFVGGKGVNLK 267

RESULT 8
Q9Y412 PRELIMINARY; PRT; 407 AA.
AC Q9Y412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp566B0846 (Fragment).
GN Name=DKFZp566B0846;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RA Ootenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PSS0835; IG-LIKE; 2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 50.4%; Score 1159.5; DB 2; Length 407;
Best Local Similarity 70.3%; Pred. No. 1.1e-81;
Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 143 SGKVICAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPV 202
Db 1 SGKVICAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPV 60

QY 203 HIDWEGDLGEMESTTTTSPNETATIIISQYKLPFTRFARGRRITCVVKGHPALEKDIRYSFI 262
Db 61 HIDWEGDLGEMESTTTTSPNETATIIISQYKLPFTRFARGRRITCVVKGHPALEKDIRYSFI 120

QY 263 LDIQYAPEVSVTYGDGNWFGVGRGVNLKCNADANPPFPKSVWSRLDQWDPGLLASDNTL 322
Db 121 LDIQYAPEVSVTYGDGNWFGVGRGVNLKCNADANPPFPKSVWSRLDQWDPGLLASDNTL 180

QY 323 HFVHPLTFNYSGVYICKVNTSLGQRSQDKVIYISDVP----- 359
Db 181 HFVHPLTFNYSGVYICKVNTSLGQRSQDKVIYISDVP----- 240

QY 360 -----FKQTSSIAVAGVIGAVLALFIAIFVTVLLTPRKK--RPSYLDKV 403
Db 241 EPKKLPFLSTLATIKDDTIATIIASVGGALFVLVSLAGIFCYRRRTFRGDYPAK- 299

QY 404 IDLPPTHKPPPLYEERSPPLPQKDLFQ 430
Db 300 -----NYIPPSDMQKES---QIDVLQ 317

RESULT 9
Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to necitin 3; DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 27.4%; Score 630.5; DB 2; Length 304;
Best Local Similarity 56.7%; Pred. No. 9.9e-41;
Matches 127; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 246 CVVKGHPALEKDIRYSFTLDIOYAPEVSVTYGDGNWFGVGRGVNLKCNADANPPFPKSVWS 305
Db 1 CVVKGHPALEKDIRYSFTLDIOYAPEVSVTYGDGNWFGVGRGVNLKCNADANPPFPKSVWS 60
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060694; AAG60694.1; -.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00408; IG2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 515 AA; 57035 MW; A56FA2C7F8B25AFB CRC64;

Query Match 25.0%; Score 575; DB 2; Length 515;
Best Local Similarity 36.4%; Pred. No. 4.1e-36;
Matches 126; Conservative 68; Mismatches 130; Indels 22; Gaps 8;

Qy 71 GKNVSLKCLIE---VNETITQISKEKHGKSKQTVAVHHPOYGFSGVQGRVLFKNYS 127
Db 44 GTDVLVLCFANPLPFSVKITQVTQWKASNGSKNNMAYNPTMTGVSFLPPEKRVFLRPS 103
Qy 128 LNDATITLHNGFSDGKYICKAVTEPLNQAQSTTVTVLVEPTVSLIKGPDLSLDG--- 184
Db 104 PIDGTIRLSGLEDEGECYCEFAFPPTGNRESQNLNTVMAKPT-NWIEGTRAVLRARKG 162
Qy 185 -GNETVAACIAATGKPVAAHLDWEGDL--GENESTTTTSPNETATISQYKLFPTFRFARGR 242
Db 163 QDDKVLVATCTSANGKPPSAVSWETRLKGEAYEIRNPNGTIVTSRYRLVPSREAHQ 222
Qy 243 RITCVWRHPALEKDIRYSFILDIOYAPESVSTGYDGNFVGRKGVNLIKCNADANPPFPFKS 302
Db 223 SLACIVNY-HLDR-FRESLTNLVQYEPVETIEGFDGNWYLQRTDVKLTCKADANPPATEY 280
Qy 303 VWSLDGQWPDGLLASNTLHVFHPLFNYSVGVICKVTNSLGRSOKYIYISDVFPKQ 362

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Db 281 HWTTLNGLPKGVEAQNRITLFFRGPIYSLAGTYICEATNPICGRSQVEVNITEPPYTP 340
Qy 363 TSS-----IAVAGAVIGAVLALFIIAIFVTVLLTPKPKRPSY 399
Db 341 TPEHGRAGQMPTAIIIGGVAGSVLLVIVVGIIIVL--RRRRHTF 384

RESULT 12
PVRL1_HUMAN STANDARD; PRT; 517 AA.
AC Q15223; O75465; O9HB66; O9HBW2;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 03-JUL-2004 (Rel. 44, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD111 antigen).
GN Name=PVRL1; Synonyms=HVEC, PRR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102; DOI=10.1016/0378-1119(94)00842-G;
RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "cDNA characterization and chromosomal localization of a gene related
RT to the poliovirus receptor gene.";
RL Gene 155:261-265 (1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127; DOI=10.1126/science.280.5369.1618;
RA Graghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
RA Spear P.G.;
RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
RT protein 1 and poliovirus receptor.";
RL Science 280:1618-1620 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA DOI=10.1128/JVI.75.12.5684-5691.2001;
RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
RA Campadelli-Fiume G., Dubreuil P.;
RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
RT nectin1 (or prr1-HIGR-Hvec) modulates positively and negatively
RT susceptibility to hsv infection.";
RL J. Virol. 75:5684-5691 (2001).
RN [4]
RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
RX MEDLINE=2032396; PubMed=10932188; DOI=10.1038/78119;
RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
RA Helms J.A., Spritz R.A.;
RT "Mutations of PVRL1, encoding a cell-cell adhesion
RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
RT dysplasia.";
RL Nat. Genet. 25:427-430 (2000).
CC -!- FUNCTION: Probably involved in cell adhesion. Receptor for
CC alphaherpesvirus (HSV-1, HSV-2 and pseudorabies virus) entry into
CC cells.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoform gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Delta;
CC IsoId=Q15223-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
CC Name=Gamma;
CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
CC ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is

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CC EMBL; AF308632; AAG30281.1; -.
CC HSPF; Q05793; IGL4.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
FT SEQUENCE 515 AA; 57047 MW; BFAB00320DD3785 CRC64;

Query Match 24.6%; Score 564.5; DB 1; Length 515;
Best Local Similarity 34.1%; Pred. No. 2.7e-35;
Matches 134; Conservative 64; Mismatches 158; Indels 37; Gaps 10;

Qy 52 LCGALAGPIIEPHVTAVGKNSLKLE---VNETITQISWEKTHGKSSQTVAVHPQ 108
Db 25 LPGAHTQVQVNDMSYGFIDGVVLCSPANPLPGVKITQVTWKATNGSKQNVAINPA 84

Qy 109 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLV 168
Db 85 MGVSVLAPYRERKVEFLRPSFTDGTIRLSRLEDEGVICFATFPAGNRESQNLTVMA 144

Qy 169 EPTVSLIKGPDSLIDG---GNETVAACIAATGKPAHIDWEGDL-GEMESTTTSPFNE 223
Db 145 KPT-NWIEGTAQVLRRAKGDVLTCTTSANGKPPSVSWETHLKGAEYQIRNPNG 203

Qy 224 TATISQYKLPPTFRFARRITCVKHPALKEKDIRYSFILDIOAPEVSVTVGYDGNWFGV 283
Db 204 TTVTISRVLPSREDHRQSLACIVNVM--DRFRESLTNVQYEPEVTIEGFDGNWYVQ 261

Qy 284 RKGYNLCNADANPPPKSVMSRLDQWPDGLASDNTLHFVHPLTFNYSVGVIKVTNS 343
Db 262 RMDVKLTCKADANPATEYHWTTLNGLSKGVEAQNRITLFFRGPIINYSMACTYICEATNP 321

Qy 344 LGORSQKVIYISDVPFFKQTS-----SIAVAGAVIGAV-LALFIIAIFVTLLTP 392
Db 322 IGTSGQVEVNITFFPYTPSPPEHCRAGQVPTAIGGVGVSILLVFWGGIVVALCRR 381

Qy 393 R-----KKR---PSYLDKVIDLPTPHKPP 413
Db 382 RHTFKGDYSTKKHVGVNGYSKAGI---PQHHP 411

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RESULT 14
Q9ERF5

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ID AC Q9ERF5 PRELIMINARY; PRT; 295 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN Name=HveC;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;
RA Milne R.S.B., Connolly S.A., Krumenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RA "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308634; AAG30283.1; -.
DR HSPF; Q05793; IGL4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 295
FT SEQUENCE 295 AA; 33112 MW; 03E5C4DCB5032E7F CRC64;

Query Match 23.2%; Score 534.5; DB 2; Length 295;
Best Local Similarity 38.3%; Pred. No. 2.8e-33;
Matches 113; Conservative 58; Mismatches 113; Indels 11; Gaps 6;

Qy 71 GKNVSLKLE---VNETITQISWEKTHGKSSQTVAVHPQYGSVQGEYQGRVLFKNYS 127
Db 3 GTDVLHCSFANPLPSVKITQVTWKATNGSKQMAIYNPTMGVSVLPPEKRVFLRPS 62

Qy 128 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVVEPTVSLIKGPDSLIDG--- 184
Db 63 FIDGTIRLSHLEDEGVICFATFPAGNRESQNLTVMAKPT-NWIEGTAQVLRRAKG 121

Qy 185 -GNETVAACIAATGKPAHIDWEGDL-GEMESTTTSPFNETATISQYKLPPTFRFARR 242
Db 122 QDDQVVVATCTSANGKPPSVSWETHLKGAEYQIRNPNGTIVTISRVLPSREAHQ 181

Qy 243 RITCVKHPALEKDIRYSFILDIOAPEVSVTVGYDGNWFGVRCGVNLCNADANPPPKFS 302
Db 182 SLACIVNY-HLDR-FRESLTNVQYEPEVTIEGFDGNWYVQRTDVKLTCKADANPATEY 239

Qy 303 VMSRLDQWPDGLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQKVIYISD 357
Db 240 HWTTLNGLSKGVEAQNRITLFFRGPIINYSLAGTYICEATNPIGTSGQVEVNITE 294

RESULT 15
Q9GL74
ID Q9GL74 PRELIMINARY; PRT; 298 AA.
AC Q9GL74
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN Name=HveC;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703; DOI=10.1006/viro.2000.0798;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 18.301 Seconds
(without alignments)
1782.508 Million cell updates/sec

Title: US-09-972-268-31
Perfect score: 2299
Sequence: 1 MATLRPSPLCPGGKQALS.....ERSPLPKDLFOVCVHEYT 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 578 | 25.1 | 458 | 4 | US-09-435-956A-1 |
| 2 | 566.5 | 24.6 | 514 | 4 | US-09-949-016-11380 |
| 3 | 566.5 | 24.6 | 517 | 4 | US-09-723-368-4 |
| 4 | 544 | 23.7 | 518 | 4 | US-09-919-172-20 |
| 5 | 465 | 20.2 | 522 | 4 | US-09-949-016-7563 |
| 6 | 458.5 | 19.9 | 479 | 4 | US-09-723-368-2 |
| 7 | 458.5 | 19.9 | 479 | 4 | US-09-949-016-6278 |
| 8 | 406 | 17.7 | 456 | 4 | US-09-949-016-7564 |
| 9 | 402 | 17.5 | 417 | 4 | US-09-949-016-6729 |
| 10 | 400.5 | 17.4 | 408 | 3 | US-09-724-864-62 |
| 11 | 306.5 | 13.3 | 442 | 4 | US-09-919-172-20 |
| 12 | 306.5 | 13.3 | 442 | 4 | US-09-930-803-1 |
| 13 | 304.5 | 13.2 | 440 | 4 | US-09-866-028-61 |
| 14 | 304.5 | 13.2 | 440 | 4 | US-09-944-457-61 |
| 15 | 290.5 | 12.6 | 423 | 4 | US-09-778-510-22 |
| 16 | 255.5 | 11.1 | 398 | 4 | US-09-778-510-4 |
| 17 | 248.5 | 10.8 | 398 | 4 | US-09-778-510-6 |
| 18 | 248.5 | 10.8 | 398 | 4 | US-09-907-794A-84 |
| 19 | 248.5 | 10.8 | 398 | 4 | US-09-905-125A-84 |
| 20 | 248.5 | 10.8 | 398 | 4 | US-09-902-775A-84 |
| 21 | 248.5 | 10.8 | 398 | 4 | US-09-906-700-84 |
| 22 | 248.5 | 10.8 | 398 | 4 | US-09-903-603A-84 |
| 23 | 248.5 | 10.8 | 398 | 4 | US-09-904-920A-84 |
| 24 | 248.5 | 10.8 | 398 | 4 | US-09-909-064-84 |
| 25 | 248.5 | 10.8 | 398 | 4 | US-09-909-381A-84 |
| 26 | 248.5 | 10.8 | 398 | 4 | US-09-906-618-84 |
| 27 | 244.5 | 10.6 | 444 | 2 | US-08-659-984A-5 |

| | | | | | | |
|----|-------|------|------|---|---------------------|-------------------|
| 28 | 244.5 | 10.6 | 444 | 3 | US-08-660-531-5 | Sequence 5, Appli |
| 29 | 238.5 | 10.4 | 432 | 4 | US-09-778-510-2 | Sequence 2, Appli |
| 30 | 237 | 10.3 | 421 | 2 | US-08-659-984A-1 | Sequence 1, Appli |
| 31 | 237 | 10.3 | 421 | 3 | US-08-660-531-1 | Sequence 2, Appli |
| 32 | 205.5 | 8.9 | 4391 | 4 | US-10-006-011A-2 | Sequence 2, Appli |
| 33 | 195 | 8.5 | 1101 | 3 | US-08-986-485-2 | Sequence 2, Appli |
| 34 | 190.5 | 8.3 | 227 | 4 | US-09-205-258-947 | Sequence 947, App |
| 35 | 187.5 | 8.2 | 274 | 3 | US-09-570-367C-19 | Sequence 19, Appl |
| 36 | 187.5 | 8.2 | 274 | 4 | US-09-915-524-19 | Sequence 19, Appl |
| 37 | 187.5 | 8.2 | 274 | 4 | US-09-934-634-19 | Sequence 19, Appl |
| 38 | 178 | 7.7 | 467 | 3 | US-09-046-736-2 | Sequence 2, Appli |
| 39 | 177 | 7.7 | 626 | 4 | US-09-949-016-6213 | Sequence 6213, Ap |
| 40 | 177 | 7.7 | 664 | 4 | US-09-949-016-7850 | Sequence 7850, Ap |
| 41 | 175 | 7.6 | 819 | 4 | US-09-949-016-11044 | Sequence 11044, A |
| 42 | 175 | 7.6 | 837 | 4 | US-09-949-016-6515 | Sequence 6515, Ap |
| 43 | 174.5 | 7.6 | 387 | 3 | US-09-175-928-2 | Sequence 2, Appli |
| 44 | 174 | 7.6 | 511 | 4 | US-09-949-016-10054 | Sequence 10054, A |
| 45 | 171.5 | 7.5 | 504 | 4 | US-09-949-016-7020 | Sequence 7020, Ap |

ALIGNMENTS

RESULT 1

US-09-435-956A-1

; Sequence 1, Application US/09435956A

; Patent No. 6469155

; GENERAL INFORMATION:

; APPLICANT: Universita degli Studi di Bologna

; APPLICANT: Institut National de la Sante et de la Recherche M

; TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a

; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and

; TITLE OF INVENTION: BHV Infections

; FILE REFERENCE: MODIANO

; CURRENT APPLICATION NUMBER: US/09/435,956A

; CURRENT FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 1

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Original Source: Hela Cell Line

; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin

; OTHER INFORMATION: Superfamily

; OTHER INFORMATION: Binding Macromolecules: HSV-gD

; OTHER INFORMATION: Subcellular localisation: Plasma Membrane

; OTHER INFORMATION: Other Information: Viral Receptor

US-09-435-956A-1

Query Match 25.1%; Score 578; DB 4; Length 458;
Best Local Similarity 35.5%; Pred. No. 2.le-47;
Matches 130; Conservative 65; Mismatches 157; Indels 14; Gaps 7;

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| Qy | 71 | GKNSVSLKLTIE---VNFTITQISWEKIHGKSSQTVAVHHPQYGFSGVQGVGRVLFKNYS | 127 |
| Db | 44 | GTDVVLHCSFANPLPSVKITQVTVQKSTNGSKQNVAINFSGMVSVLAPYRVERFLRPS | 103 |
| Qy | 128 | LDNATITLHNIIGSDSGKIYCKAVTFPLGNAQSTTTVTLVETVSLIKGPDSDLIDG--- | 184 |
| Db | 104 | FTDGTIRLSRLLEDEGVYICGFATFPTNGRESQNLNTVMKPT--NWIEGTQAVLRKKG | 162 |
| Qy | 185 | -GNETVAICIAATGKPAVIDWEGDL--GEMESTTTSFPNETATIIISQYKLFPTFRFARG | 242 |
| Db | 163 | ODDKVLVATCTISANGKPPSVVSWETRLKGAEYQIEINPNTGTVTVISRYRLVPSREAHQ | 222 |
| Qy | 243 | RITCVWXPALFKDIRYSFLIDIQAYEVSVTGVDGNWFGVGRKGVNLKCNADANPPFPKS | 302 |
| Db | 223 | SLACIVNYHM--DRFKESLTINQYEFVETIEGFDGNWYLRQMDVKLTCKADANPPATEY | 280 |
| Qy | 303 | VWSRLDQGWDPGLIASDNTLHFVHPLFTNYSVGVIKVTNSLQORSQKVIISDVFPKQ | 362 |

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Db 281 HWTTLNGLSLPKGVGAQNRTLFFKGPINYSLAGTYICEATNPICTRSGQVEVNITEPRPQ 340
QY 363 TSSIAVAGAVIGAVLAFIIFVTV--LLTPRKRPYSYLDKV-IDLPPTHKPPPLYEER 419
Db 341 RGLGSAARLLAGTAVFLIILVAVTVFLFLNROOKSPPTDGTGAGTQDPLSQKPEPSRQ 400
QY 420 SPLPLPQ 425
Db 401 SSLVPE 406

RESULT 2
US-09-949-016-11380
; Sequence 11380, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11380
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11380

Query Match 24.6%; Score 566.5; DB 4; Length 514;
Best Local Similarity 35.2%; Pred. No. 3.4e-46;
Matches 122; Conservative 68; Mismatches 134; Indels 23; Gaps 7;

QY 71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGEYQGRVLFKNYS 127
Db 41 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSLAPYRVERVEFLRPS 100
QY 128 LNDATITLHNGSDSKYICKAVTTPPLGNAQSSTTVTLVPTVSLIKGPDLSLDG--- 184
Db 101 FTDGTLRLSLEDEGVYICEFATPPTGNRESQNLNLTVMKPT-NWIEGTQAVLRAKKG 159
QY 185 -GNETVAACIAATGKPVAHIDWEGDL-GEMESTTTTSFPNETATIIISQYKLPFTRFARGR 242
Db 160 QDDKVLVATCTSANGKPPSVSVSWETRLKGEAEYQEIENPNGTVTVISRYLVSREAHQ 219
QY 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGDGNFWVGRKGVNLCNADANPPFPKS 302
Db 220 SLACIVNYHM--DRFKESLTNLVQVEPEVTIEGFDGNWYLQRMVDVLTCKADANPPATEY 277
QY 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQKVIYISDVPPFKQ 362
Db 278 HWTTLNGLSLPKGVGAQNRTLFFKGPINYSLAGTYICEATNPICTRSGQVEVNITEPPTP 337
QY 363 TS-----SIAVAGAVIGAVLAFIIFVTVLLTPRKRPSPY 399
Db 338 SPPEHGRAGPVPTAIGGVAGSILLVIVGGIVVAL--RRRHPTP 382

RESULT 3
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
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; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITEBECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1998-06-03
; PRIOR FILING DATE: 1999-06-02
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match 24.6%; Score 566.5; DB 4; Length 517;
Best Local Similarity 35.2%; Pred. No. 3.4e-46;
Matches 122; Conservative 68; Mismatches 134; Indels 23; Gaps 7;

QY 71 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFSGVQGEYQGRVLFKNYS 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSLAPYRVERVEFLRPS 103
QY 128 LNDATITLHNGSDSKYICKAVTTPPLGNAQSSTTVTLVPTVSLIKGPDLSLDG--- 184
Db 104 FTDGTLRLSLEDEGVYICEFATPPTGNRESQNLNLTVMKPT-NWIEGTQAVLRAKKG 162
QY 185 -GNETVAACIAATGKPVAHIDWEGDL-GEMESTTTTSFPNETATIIISQYKLPFTRFARGR 242
Db 163 QDDKVLVATCTSANGKPPSVSVSWETRLKGEAEYQEIENPNGTVTVISRYLVSREAHQ 222
QY 243 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGDGNFWVGRKGVNLCNADANPPFPKS 302
Db 223 SLACIVNYHM--DRFKESLTNLVQVEPEVTIEGFDGNWYLQRMVDVLTCKADANPPATEY 280
QY 303 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQKVIYISDVPPFKQ 362
Db 281 HWTTLNGLSLPKGVGAQNRTLFFKGPINYSLAGTYICEATNPICTRSGQVEVNITEPPTP 340
QY 363 TS-----SIAVAGAVIGAVLAFIIFVTVLLTPRKRPSPY 399
Db 341 SPPEHGRAGPVPTAIGGVAGSILLVIVGGIVVAL--RRRHPTP 385

RESULT 4
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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[illegible]

; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

Query Match 12.6%; Score 290.5; DB 4; Length 423;
Best Local Similarity 25.7%; Pred. No. 1.7e-19;
Matches 102; Conservative 71; Mismatches 165; Indels 59; Gaps 14;

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| Qy | 36 | PPPL-LLLLPPLLFSLRCLGALAGPIIVEPHVTAVMGKNVSLKCLIEVNETITQISWEKI | 94 |
| Db | 3 | PPGLRLRLLLLLLSAALITPGDQNLFTKDVTVIEGEVATISC-QVNKSDDSVI--QL | 58 |
| Qy | 95 | HGKSSQTVAVHHPOYGFSGVQGYGVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFP | 154 |
| Db | 59 | LNPNRQTI-----YPRDFRPLKDSRFQLNFSSELKSVSLTNVSIISDEGRYFCQLYTDP | 112 |
| Qy | 155 | LGNAQSSTTVTLVEPTVSLIK-GPDSLIDGNETVAAICIAATGKPVAHIDW-EGD--- | 209 |
| Db | 113 | --POESYTTITVLVPPRNLMIDIOKDTAVEG--EEIEVNCNTAMASKPATTIRWFKGNKEL | 168 |
| Qy | 210 | --LGEMESTTTSFENETATISQVKLFTPTFARGRRITCVVKHPALEKDIRYSFILDIQY | 267 |
| Db | 169 | KGKSEVEWSDMY-----TVTSQMLKVKHEDDGVVICQVEHPAVTGNLQORYLEVQY | 223 |
| Qy | 268 | APEVSVTGYDGNWFVGRKG--VNLKCNADANPPPKSVNSRLDQWPDGLASDNTLHFV | 325 |
| Db | 224 | KPQVHIQMTYPLQGLTREGDAFELTCEAIGKQPVMVTWVRVDDMPQHAVLSGNL-FI | 282 |
| Qy | 326 | HPLTFNYSGVYICKVNSLQORSQKVIYISDVP-----FKOTSSI----- | 366 |
| Db | 283 | NNLKNKTGTYRCBASINVGKASHSDYMLYVYDPTTTPPTTTTTTTTTTTTTTTTTITD | 342 |
| Qy | 367 | -----AVAGAVIGAVLALFIIAIFVTVLLTPR | 393 |
| Db | 343 | SRAGEGTIGAVDHAVIGGVAVVVFAMLCLLIILGR | 379 |

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Job time : 19.301 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2005, 09:13:38 ; Search time 203.192 Seconds
(without alignments)
894.712 Million cell updates/sec

Title: US-09-972-268-31
Perfect score: 2299
Sequence: 1 MARTLRPSPLCPGGGKAQLS.....ERSPPLPKDOLFQVCVHEYT 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 2299 | 100.0 | 437 | 10 | US-09-972-268-31 |
| 2 | 2257 | 98.2 | 510 | 10 | US-09-972-268-12 |
| 3 | 2243 | 97.6 | 510 | 10 | US-09-972-268-10 |
| 4 | 2229 | 97.0 | 504 | 10 | US-09-972-268-8 |
| 5 | 2108 | 91.7 | 510 | 10 | US-09-959-845-4 |
| 6 | 2108 | 91.7 | 510 | 10 | US-09-972-268-18 |
| 7 | 2107 | 91.6 | 438 | 10 | US-09-959-845-6 |
| 8 | 2107 | 91.6 | 438 | 10 | US-09-972-268-19 |
| 9 | 1912 | 83.2 | 387 | 10 | US-09-972-268-16 |
| 10 | 1912 | 83.2 | 595 | 10 | US-09-972-268-14 |
| 11 | 1902.5 | 82.8 | 549 | 10 | US-09-972-268-6 |
| | | | | | Sequence 31, Appl |
| | | | | | Sequence 12, Appl |
| | | | | | Sequence 10, Appl |
| | | | | | Sequence 8, Appl |
| | | | | | Sequence 4, Appl |
| | | | | | Sequence 18, Appl |
| | | | | | Sequence 6, Appl |
| | | | | | Sequence 19, Appl |
| | | | | | Sequence 16, Appl |
| | | | | | Sequence 14, Appl |
| | | | | | Sequence 6, Appl |

| | | | | | | |
|----|--------|------|-----|----|-------------------|--------------------|
| 12 | 1902.5 | 82.8 | 549 | 14 | US-10-161-572-45 | Sequence 45, Appl |
| 13 | 1888.5 | 82.1 | 549 | 10 | US-09-972-268-4 | Sequence 4, Appl |
| 14 | 1879 | 81.7 | 634 | 10 | US-09-972-268-13 | Sequence 13, Appl |
| 15 | 1878 | 81.7 | 426 | 10 | US-09-972-268-15 | Sequence 15, Appl |
| 16 | 1867.5 | 81.2 | 542 | 10 | US-09-972-268-2 | Sequence 2, Appl |
| 17 | 1803 | 78.4 | 549 | 10 | US-09-959-845-2 | Sequence 2, Appl |
| 18 | 1803 | 78.4 | 549 | 10 | US-09-972-268-17 | Sequence 17, Appl |
| 19 | 581 | 25.3 | 458 | 10 | US-09-972-268-21 | Sequence 21, Appl |
| 20 | 566.5 | 24.6 | 514 | 14 | US-10-161-572-60 | Sequence 20, Appl |
| 21 | 566.5 | 24.6 | 517 | 10 | US-09-972-268-20 | Sequence 20, Appl |
| 22 | 544 | 23.7 | 518 | 9 | US-09-919-172-20 | Sequence 20, Appl |
| 23 | 544 | 23.7 | 518 | 16 | US-10-752-986-20 | Sequence 20, Appl |
| 24 | 526 | 22.9 | 510 | 15 | US-10-422-571-5 | Sequence 5, Appl |
| 25 | 526 | 22.9 | 510 | 15 | US-10-422-571-31 | Sequence 31, Appl |
| 26 | 522 | 22.7 | 485 | 15 | US-10-422-571-15 | Sequence 15, Appl |
| 27 | 522 | 22.7 | 485 | 15 | US-10-422-571-33 | Sequence 33, Appl |
| 28 | 522 | 22.7 | 485 | 15 | US-10-422-571-114 | Sequence 114, Appl |
| 29 | 522 | 22.7 | 485 | 15 | US-10-422-571-116 | Sequence 116, Appl |
| 30 | 522 | 22.7 | 485 | 15 | US-10-422-571-129 | Sequence 129, Appl |
| 31 | 522 | 22.7 | 497 | 10 | US-09-972-268-37 | Sequence 37, Appl |
| 32 | 522 | 22.7 | 510 | 10 | US-09-766-511B-33 | Sequence 33, Appl |
| 33 | 522 | 22.7 | 510 | 14 | US-10-241-220-94 | Sequence 94, Appl |
| 34 | 522 | 22.7 | 510 | 15 | US-10-295-027-66 | Sequence 66, Appl |
| 35 | 522 | 22.7 | 510 | 15 | US-10-173-999-76 | Sequence 76, Appl |
| 36 | 522 | 22.7 | 510 | 15 | US-10-058-270A-54 | Sequence 54, Appl |
| 37 | 522 | 22.7 | 510 | 15 | US-10-188-832-179 | Sequence 179, Appl |
| 38 | 522 | 22.7 | 510 | 15 | US-10-422-571-3 | Sequence 3, Appl |
| 39 | 522 | 22.7 | 510 | 15 | US-10-422-571-7 | Sequence 7, Appl |
| 40 | 522 | 22.7 | 510 | 15 | US-10-422-571-9 | Sequence 9, Appl |
| 41 | 522 | 22.7 | 510 | 15 | US-10-422-571-11 | Sequence 11, Appl |
| 42 | 522 | 22.7 | 510 | 15 | US-10-422-571-17 | Sequence 17, Appl |
| 43 | 522 | 22.7 | 510 | 15 | US-10-422-571-25 | Sequence 25, Appl |
| 44 | 522 | 22.7 | 510 | 15 | US-10-422-571-30 | Sequence 30, Appl |
| 45 | 522 | 22.7 | 510 | 15 | US-10-422-571-36 | Sequence 36, Appl |

ALIGNMENTS

RESULT 1

US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

| | | | | |
|-----------------------|-----------------|--|-----------|-------------|
| Query Match | 100.0%; | Score 2299; | DB 10; | Length 437; |
| Best Local Similarity | 100.0%; | Pred. No. 1.1e-168; | | |
| Matches 437; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | MARTLRPSPLCPGGGKAQLSSALGAGLLQLQPTPPPLLLLPPLLLFRLCCALAGPI | 60 | |
| Db | 1 | MARTLRPSPLCPGGGKAQLSSALGAGLLQLQPTPPPLLLLPPLLLFRLCCALAGPI | 60 | |
| Qy | 61 | IVPHTVAVGKGVSLKCLIEVNETTQISWEKHSSQTVAVHHPOYCFSGVQGR | 120 | |

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Db      61  IVEPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Qy      121  VLFKNYSLNDATTILHNIGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db      121  VLFKNYSLNDATTILHNIGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy      181  LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATTISQYKLFPTFRFAR 240
Db      181  LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATTISQYKLFPTFRFAR 240
Qy      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Db      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Qy      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Db      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Qy      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Qy      421  PPLPQKDLFQVCVHEYT 437
Db      421  PPLPQKDLFQVCVHEYT 437

RESULT 2
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972.268
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match      98.2%; Score 2257; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.3e-165;
Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MARTLRSPICPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLRLCGALAGPI 60
Db      1  MARTLRSPICPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLRLCGALAGPI 60
Qy      61  IVEPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Db      61  IVEPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Qy      121  VLFKNYSLNDATTILHNIGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db      121  VLFKNYSLNDATTILHNIGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy      181  LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATTISQYKLFPTFRFAR 240
Db      181  LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATTISQYKLFPTFRFAR 240
Qy      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Db      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Qy      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Db      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Qy      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Qy      421  PPLPQKDLFQVCVHEYT 437
Db      421  PPLPQKDLFQVCVHEYT 437
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Db      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Qy      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Db      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Qy      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Qy      421  PPLPQKDLFQ 430
Db      421  PPLPQKDLFQ 430

RESULT 3
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match      97.6%; Score 2243; DB 10; Length 510;
Best Local Similarity 99.5%; Pred. No. 2.8e-164;
Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MARTLRSPICPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLRLCGALAGPI 60
Db      1  MARTLRSPICPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLRLCGALAGPI 60
Qy      61  IVEPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Db      61  IVEPHVTAVWGKNSLKLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSGVQYQGR 120
Qy      121  VLFKNYSLNDATTILHNIGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db      121  VLFKNYSLNDATTILHNIGSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy      181  LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATTISQYKLFPTFRFAR 240
Db      181  LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPNETATTISQYKLFPTFRFAR 240
Qy      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Db      241  GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF 300
Qy      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Db      301  KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPF 360
Qy      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db      361  KOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
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Qy 421 PPLPQKDLFQ 430
|||||
Db 421 PPLPQKDLFQ 430

RESULT 4

US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match 97.0%; Score 2229; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.3e-163;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PSLPCPGGKAQLSSASLLGAGLLQLPPTPPLLLLLPPLLLFSLRCLGALAGPIIVPHV 66
Db 1 PSLPCPGGKAQLSSASLLGAGLLQLPPTPPLLLLLPPLLLFSLRCLGALAGPIIVPHV 60

Qy 67 TAVGKNVSKCLLEVNETITQISWEKIHGKSSQTVAHHPOYGFSGVQGYQGRVLFKNY 126
Db 61 TAVGKNVSKCLLEVNETITQISWEKIHGKSSQTVAHHPOYGFSGVQGYQGRVLFKNY 120

Qy 127 SLNDATITLHNIGFSDGKYICKAVTTPPLGNAQSTTTVLVEPTVSLIKGPDSLIDGN 186
Db 121 SLNDATITLHNIGFSDGKYICKAVTTPPLGNAQSTTTVLVEPTVSLIKGPDSLIDGN 180

Qy 187 ETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRITC 246
Db 181 ETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRITC 240

Qy 247 VVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPKSVMSR 306
Db 241 VVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPKSVMSR 300

Qy 307 LDGQWPDGLASDNTLHFVHPLTNYSGVIYCKVTNSLGQRSDQKVIYISDVPPKQTSII 366
Db 301 LDGQWPDGLASDNTLHFVHPLTNYSGVIYCKVTNSLGQRSDQKVIYISDVPPKQTSII 360

Qy 367 AVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQK 426
Db 361 AVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERSPPLPQK 420

Qy 427 DLQK 430
|||||
Db 421 DLQK 424

RESULT 5

US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US2003008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI

; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4

Query Match 91.7%; Score 2108; DB 10; Length 510;
Best Local Similarity 92.2%; Pred. No. 7.1e-154;
Matches 400; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MARTLRPSLPCPGGKAQLSSASLLGAGLLQLPPTPPLLLLLPPLLLFSLRCLGALAGPI 60
Db 1 MARTPGPAPLPCPGGKAQLSSAFPPAAGLLLPAPTPPPLLLLLLPLLLFSLRCLGALAGSI 60

Qy 61 IVEPHVTAVMGKNVSKCLLEVNETITQISWEKIHGKSSQTVAHHPOYGFSGVQGYQGR 120
Db 61 IVEPHVTAVMGKNVSKCLLEVNETITQISWEKIHGKSTQTVAHHPOYGFSGVQGYQGR 120

Qy 121 VLFKNYSLNDATITLHNIGFSDGKYICKAVTTPPLGNAQSTTTVLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATITLHNIGFSDGKYICKAVTTPPLGNAQSTTTVLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACVAAATGKPVAAQIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240

Qy 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNMFVGRKGVNLCNADANPPPF 300

Qy 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTNYSGVIYCKVTNSLGQRSDQKVIYISDVPP 360
Db 301 KSVMSRLDGQWPDGLASDNTLHFVHPLTNYSGVIYCKVSNLSGQRSDQKVIYISDIPL 360

Qy 361 KQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
Db 361 TOTSSIAVAGAVIGAVLAFIITVFTVLLTPRKRPSYLDKVIDLPPTHKPPPLYEERI 420

Qy 421 PPLPQKDLFQVCVH 434
|||||
Db 421 PSUPQKDLGQTEH 434

RESULT 6

US-09-972-268-18
; Sequence 18, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 510
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-18

Query Match          91.7%; Score 2108; DB 10; Length 510;
Best Local Similarity 92.2%; Pred. No. 7.1e-154;
Matches 400; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLFRLCGALAGPI 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARTPGAPLCPGGGKAQLSSAPPAAGLLLPAPTTPPLLLLPFLFRLCGALAGSI 60

QY 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGYQGR 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGYQGR 120

QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFAR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFAR 240

QY 241 GRITCVCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 GRITCVCVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300

QY 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPF 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 KSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPF 360

QY 361 KOTSSIAVAGAVIGAVLALFIITVTLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 KOTSSIAVAGAVIGAVLALFIITVTLTPRKRPSYLDKVIDLPPTHKPPPLYEERS 420

QY 421 PPLPQKDL 438
Db 421 PSLPQKDL 428

RESULT 8
US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 438
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

Query Match          91.6%; Score 2107; DB 10; Length 438;
Best Local Similarity 93.2%; Pred. No. 7e-154;
Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLFRLCGALAGPI 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MARTPGAPLCPGGGKAQLSSAPPAAGLLLPAPTTPPLLLLPFLFRLCGALAGSI 60

QY 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGYQGR 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGYQGR 120

QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180

Query Match          91.6%; Score 2107; DB 10; Length 438;
Best Local Similarity 93.2%; Pred. No. 7e-154;
Matches 399; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 MARTLRPSPLCPGGGKAQLSSASLLGAGLLLOPPTPPPLLLLPFLFRLCGALAGPI 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MARTPGAPLCPGGGKAQLSSAPPAAGLLLPAPTTPPLLLLPFLFRLCGALAGSI 60

QY 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGYQGR 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGYQGR 120

QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 180
```


| | | | |
|--|-----|---|-----|
| Qy | 181 | LIDGNETVAACIAATCKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR | 240 |
| Db | 181 | LIDGNETVAACIAATCKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR | 240 |
| Qy | 241 | GRITCVVKHPALEKDIRYSFLDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Db | 241 | GRITCVVKHPALEKDIRYSFLDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Qy | 301 | KSVNSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYIICKVNSLSGORSQDKVIYISDVPF | 360 |
| Db | 301 | KSVNSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYIICKVNSLSGORSQDKVIYISDVPF | 360 |
| Qy | 361 | KOTSSIAVAGAVIGAVLALFIATFVTLTPRKRPSVLDKVIDLPTHKPPPIYESS | 420 |
| Db | 361 | TQTSIAVAGAVIGAVLALFIITVFVTLTPRKRPSVLDKVIDLPTHKPPPIYESS | 420 |
| Qy | 421 | PPLPQKDL 428 | |
| Db | 421 | PSLPQKDL 428 | |
| <p>RESULT 9</p> <p>US-09-972-268-16</p> <p>; Sequence 16, Application US/09972268</p> <p>; Publication No. US2003004893A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Baum, Peter R.</p> <p>; APPLICANT: Fanslow, William C.</p> <p>; APPLICANT: Lofton, Timothy E.</p> <p>; APPLICANT: Sorensen, Eric A.</p> <p>; APPLICANT: Youakim, Adel</p> <p>; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING</p> <p>; FILE REFERENCE: 3101-A</p> <p>; CURRENT APPLICATION NUMBER: US/09/972,268</p> <p>; CURRENT FILING DATE: 2001-10-05</p> <p>; PRIOR APPLICATION NUMBER: 60/238,557</p> <p>; PRIOR FILING DATE: 2000-10-05</p> <p>; NUMBER OF SEQ ID NOS: 39</p> <p>; SOFTWARE: PatentIn version 3.1</p> <p>; SEQ ID NO 16</p> <p>; LENGTH: 387</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Artificial Sequence</p> <p>; FEATURE:</p> <p>; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis</p> <p>US-09-972-268-16</p> | | | |
| <p>Query Match 83.2%; Score 1912; DB 10; Length 387;</p> <p>Best Local Similarity 99.5%; Pred. No. 6.4e-139;</p> <p>Matches 363; Conservative 0; Mismatches 2; Indels 0; Gaps 0</p> | | | |
| Qy | 1 | MARTLPSPCLPGGGKAQLSSASLLGALLQPTPPPLLLLLFPLLLSRLCGALAGPI | 60 |
| Db | 1 | MARTPGSPCLPGGGKAQLSSASLLGALLQPTPPPLLLLLFPLLLSRLCGALAGPI | 60 |
| Qy | 61 | IVEPHVAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFVSQGEYQGR | 120 |
| Db | 61 | IVEPHVAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFVSQGEYQGR | 120 |
| Qy | 121 | VLFNYSNDATITLHNTGFSDSGKYICKAVTFPLGNAQSSSTVTVLVEPTVSLIKGPD | 180 |
| Db | 121 | VLFNYSNDATITLHNTGFSDSGKYICKAVTFPLGNAQSSSTVTVLVEPTVSLIKGPD | 180 |
| Qy | 181 | LIDGNETVAACIAATCKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR | 240 |
| Db | 181 | LIDGNETVAACIAATCKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR | 240 |
| Qy | 241 | GRITCVVKHPALEKDIRYSFLDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Db | 241 | GRITCVVKHPALEKDIRYSFLDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Qy | 301 | KSVNSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYIICKVNSLSGORSQDKVIYISDVPF | 360 |

APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
PRIORITY FILING DATE: 2001-10-05
PRIORITY FILING DATE: 2000-10-05
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent in version 3.1
SEQ ID NO 6
LENGTH: 549
TYPE: PRT
ORGANISM: homo sapiens
US-09-972-268-6

Query Match 82.8%; Score 1902.5; DB 10; Length 549;
Best Local Similarity 79.3%; Pred. No. 5.4e-138;
Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLQPTPPPLLLLLFPPLLLFRLCGALAGPI 60
DB 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLQPTPPPLLLLLFPPLLLFRLCGALAGPI 60
QY 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEYQGR 120
DB 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPDS 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPDS 180
QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
DB 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
QY 241 GRITCVVHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
DB 241 GRITCVVHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVP- 359
DB 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPT 360
QY 360 -----FKQTSSTAVAGAVIGAVIALFIIA 383
DB 361 TTTLQPTIQWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGALFIVLVS 420
QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPLPQKDLFQ 430
DB 421 VLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES----QIDVLQ 459

RESULT 12
US-10-161-572-45
Sequence 45, Application US/10161572
Publication No. US20030087266A1
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-097C-PC
CURRENT APPLICATION NUMBER: US/10/161,572
CURRENT FILING DATE: 2002-06-03
PRIORITY FILING DATE: US 60/296,076
PRIORITY FILING DATE: 2001-06-05
PRIORITY FILING DATE: US 60/328,605
PRIORITY FILING DATE: 2001-10-10
PRIORITY FILING DATE: US 60/338,733
PRIORITY FILING DATE: 2001-10-22
PRIORITY FILING DATE: US 60/357,253
PRIORITY FILING DATE: 2002-02-15
PRIORITY FILING DATE: US 60/357,600

PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent in version 3.1
SEQ ID NO 45
LENGTH: 549
TYPE: PRT
ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 82.8%; Score 1902.5; DB 14; Length 549;
Best Local Similarity 79.3%; Pred. No. 5.4e-138;
Matches 372; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLQPTPPPLLLLLFPPLLLFRLCGALAGPI 60
DB 1 MARTLRPSPLCPGGKAQLSSASLLGAGLLQLQPTPPPLLLLLFPPLLLFRLCGALAGPI 60
QY 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEYQGR 120
DB 61 IVEPHVTAVMGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPDS 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTVTLVEPTVSLIKGPDS 180
QY 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
DB 181 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFAR 240
QY 241 GRITCVVHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
DB 241 GRITCVVHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 300
QY 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVP- 359
DB 301 KSVMSRLDGOWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPT 360
QY 360 -----FKQTSSTAVAGAVIGAVIALFIIA 383
DB 361 TTTLQPTIQWHPSTADIEDLATEPKLPPLSLTLATIKDDTIATIIASVVGALFIVLVS 420
QY 384 IFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPLPQKDLFQ 430
DB 421 VLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES----QIDVLQ 459

RESULT 13
US-09-972-268-4
Sequence 4, Application US/09972268
Publication No. US20030044893A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIORITY FILING DATE: 2001-10-05
PRIORITY FILING DATE: 2000-10-05
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent in version 3.1
SEQ ID NO 4
LENGTH: 549
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from human Nectin-3 alpha
US-09-972-268-4

```
Query Match      82.1%; Score 1888.5; DB 10; Length 549;
Best Local Similarity 78.9%; Pred. No. 6.5e-137;
Matches 370; Conservative 16; Mismatches 34; Indels 49; Gaps 4;

Qy 1 MARTLRPSPLCPGGGKAQLSSASLLGALLLQPTPPPLLLLPFLLLFSLRCGALAGPI 60
Db 1 MARTPGSPPLCPGGGKAQLSSASLLGALLLQPTPPPLLLLPFLLLFSLRCGALAGPI 60

Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120
Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120

Qy 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTEPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTEPLGNAQSSTTVTLVEPTVSLIKGPD 180

Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR 240

Qy 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGVNLCNADANPPPF 300

Qy 301 KSVMSRLDGOQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
Db 301 KSVMSRLDGOQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360

Qy 360 -----FKQTSSIAVAGAVICAVLALFIIA 383
Db 361 TTTTQTIQHPSTADIEDLATEPKLPPPLSTLATIKDDTIATIASVGGALFIVLS 420

Qy 384 IFVTVLTPRK--RPSYLDKVIDLPPTHKPPPYEERSPPLPQKDLFQ 430
Db 421 VLAGIFCYRRRTFRGDFYAK-----NYIPSDMQKES-----QIDVLQ 459

RESULT 14
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match      81.7%; Score 1879; DB 10; Length 634;
Best Local Similarity 83.1%; Pred. No. 4.2e-136;
Matches 373; Conservative 6; Mismatches 38; Indels 32; Gaps 4;

Qy 1 MARTLRPSPLCPGGGKAQLSSASLLGALLLQPTPPPLLLLPFLLLFSLRCGALAGPI 60
Db 1 MARTPGSPPLCPGGGKAQLSSASLLGALLLQPTPPPLLLLPFLLLFSLRCGALAGPI 60

Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120
Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120
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Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120
Qy 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTEPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTEPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR 240
Qy 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGVNLCNADANPPPF 300
Db 241 GRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTVGYDGNMFVGRKGVNLCNADANPPPF 300
Qy 301 KSVMSRLDGOQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
Db 301 KSVMSRLDGOQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIVISDVPF 360
Qy 361 KQTSSIAVAGAVICAVLALFIIAIFVTVLATPCKRPSYL-----DKVI 404
Db 361 TTT-----LQPTIOWHPSTADIEDLATEPKLPPPLSTLATIKDDTIATRSCKRTH 411
Qy 405 DLPPTHKP-----PPLYEERSPPLPQKDL 428
Db 412 TCPCPAPEAEGAPSVF--LFPPKPKDTL 438

RESULT 15
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match      81.7%; Score 1878; DB 10; Length 426;
Best Local Similarity 98.3%; Pred. No. 3e-136;
Matches 357; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARTLRPSPLCPGGGKAQLSSASLLGALLLQPTPPPLLLLPFLLLFSLRCGALAGPI 60
Db 1 MARTPGSPPLCPGGGKAQLSSASLLGALLLQPTPPPLLLLPFLLLFSLRCGALAGPI 60

Qy 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120
Db 61 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVOGEYQGR 120

Qy 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTEPLGNAQSSTTVTLVEPTVSLIKGPD 180
Db 121 VLFKNYSLNDATTILHNIGFSDSGKYICKAVTEPLGNAQSSTTVTLVEPTVSLIKGPD 180
Qy 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR 240
Db 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFAR 240
```

| | | | |
|----|-----|--|-----|
| Qy | 241 | GREITCVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Db | 241 | GREITCVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPF | 300 |
| Qy | 301 | KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQKVYIISDVPP | 360 |
| Db | 301 | KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQKVYIISDPPT | 360 |
| Qy | 361 | KQT | 363 |
| Db | 361 | TTT | 363 |

Search completed: October 6, 2005, 09:33:48
Job time : 205.192 secs

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OM protein - protein search, using sw model

Run on: October 7, 2005, 14:07:37 ; Search time 0.001 Seconds
(without alignments)
821.853 Million cell updates/sec

Title: US-09-972-268-6
Perfect score: 2901
Sequence: 1 MARTLRPSPFCGGGKAQLS.....EDDLVSHVDGVSISRREYV 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 1497 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : US09959845-2-4-6:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-------------------|-------------------|
| 1 | 2721 | 93.8 | 549 | 1 US-09-959-845-2 | Sequence 2, Appli |
| 2 | 1814.5 | 62.5 | 510 | 1 US-09-959-845-4 | Sequence 4, Appli |
| 3 | 1809.5 | 62.4 | 438 | 1 US-09-959-845-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
US-09-959-845-2
; Sequence 2, Application US/09959845
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-2

Query Match 93.8%; Score 2721; DB 1; Length 549;

Best Local Similarity 92.9%; Pred. No. 0;
Matches 510; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
QY 1 MARTLRPSPFCGGGKAQLSSASLIGALLLPPTPPPLLLLPFLSRLCGALAGPI 60
DB 1 MARTPGAPLCPGGGKAQLSSAFPPAAGLLLPAPTTPPLLLLIPLLSRLCGALAGSI 60
QY 61 IVEPHVTAVWGKNSLKLCLIEVNETITQISWEKIHGKSQTAVVHHHPQGFSGVQSGYQGR 120
DB 61 IVEPHVTAVWGKNSLKLCLIEVNETITQISWEKIHGKSQTAVVHHHPQGFSGVQSGYQGR 120
QY 121 VLFKNYSLNDATITLHNIGFSDSGYKICAVTFPLGNAQSSSTTVTLVPTVSLIKGPDS 180
DB 121 VLFKNYSLNDATITLHNIGFSDSGYKICAVTFPLGNAQSSSTTVTLVPTVSLIKGPDS 180
QY 181 LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFAR 240
DB 181 LIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFAR 240
QY 241 GRRITCVVKHPALEKDIIRYSFILDIOYAPEVSVTGYDGNWFGVRKGVNLKCNADANPPPF 300
DB 241 GRRITCVVKHPALEKDIIRYSFILDIOYAPEVSVTGYDGNWFGVRKGVNLKCNADANPPPF 300
QY 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNTSGVYICKVTNSLQORSQDKVIYISDPPT 360
DB 301 KSVWSRLDQWPDGLLASDNTLHFVHPLTFNTSGVYICKVTNSLQORSQDKVIYISDPPT 360
QY 361 TTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFLVLVS 420
DB 361 TTTLOPTQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFLVLVS 420
QY 421 VIAGIFCYRRRTFRGDYFKNYIIPSDMQKESQIDVLQOQDELSDYPSVKENKKNPVNN 480
DB 421 VIAGIFCYRRRTFRGDYFKNYIIPSDMQKESQIDVLQOQDELSDYPSVKENKKNPVNN 480
QY 481 LIRKDYLEPEKTONNVNENLFRPMDYIEDLKGMKFKVSDHEVDENEDDVLVSHVDGS 540
DB 481 LIRKDYLEPEKTONNVNENLFRPMDYIEDLKGMKFKVSDHEVDENEDDVLVSHVDGS 540
QY 541 VISRREYV 549
DB 541 VISRREYV 549
RESULT 2
US-09-959-845-4
; Sequence 4, Application US/09959845
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4
Query Match 62.5%; Score 1814.5; DB 1; Length 510;
Best Local Similarity 66.4%; Pred. No. 0;
Matches 374; Conservative 39; Mismatches 83; Indels 67; Gaps 10;
QY 1 MARTLRPSPFCGGGKAQLSSASLIGALLLPPTPPPLLLLPFLSRLCGALAGPI 60

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Db      1  MARTPGAPLCPGGKRAQLSSAFPPAAGLLLPAPTPPPLLLLPALLSRLCGALAGSI 60
QY      61  IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGYQGR 120
Db      61  IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGYQGR 120
QY      121  VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPPS 180
Db      121  VLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPPS 180
QY      181  LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRAR 240
Db      181  LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRAR 240
QY      241  GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPPF 300
Db      241  GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPPF 300
QY      301  KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTSNLSGORSQKVIYISDPPT 360
Db      301  KSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTSNLSGORSQKVIYISDPL 360
QY      361  TTTLOPTIQWHPSTADIEDLATEPKKLPPPLSTLATIKDDTIATIIASVVGALFIVLVS 420
Db      361  TQT-----SSIA-----VAGAVIGAVLALFIIT 383
QY      421  VLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK---ESQIDVLQODEL 463
Db      384  VFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPVYEEIRPSLPQKDL 428

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Search completed: October 7, 2005, 14:07:38
Job time : 1 secs

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RESULT 3
US-09-959-845-6
; Application US/09959845
; GENERAL INFORMATION: TAKAI
; APPLICANT: Yoshimi NAKANISHI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

Query Match      62.4%; Score 1809.5; DB 1; Length 438;
Best Local Similarity 76.2%; Pred. No. 0;
Matches 356; Conservative 25; Mismatches 43; Indels 43; Gaps 5;

QY      1  MARTLRPSPLCPGGKRAQLSSALLGAGLLLPPTPPPLLLLPALLSRLCGALAGPI 60
Db      1  MARTPGAPLCPGGKRAQLSSAFPPAAGLLLPAPTPPPLLLLPALLSRLCGALAGSI 60
QY      61  IVEPHVTAVGKGNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGYQGR 120

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Query Match 77.8%; Score 2107; DB 1; Length 438;
Best Local Similarity 93.2%; Pred. No. 0;

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Db      61  IVEPHVTAWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDYQGR 120
      121  VLFKNYSLNDATITLHNIGFSDSGKVIKAVTTPPLGNAQSSTTVTLVPTVSLIKGPD 180
      121  VLFKNYSLNDATITLHNIGFSDSGKVIKAVTTPPLGNAQSSTTVTLVPTVSLIKGPD 180
      181  LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISOYKLFPTFRFAR 240
      181  LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISOYKLFPTFRFAR 240
      241  GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
      241  GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
      301  KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVIYISDVPP 360
      301  KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVIYISDIPL 360
      361  KOTSSIAVAGAVIGAVLALFIITAVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERS 420
      361  TOTSSIAVAGAVIGAVLALFIITAVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYEERI 420
      421  PPLPQKDL 428
      421  PSLPQKDL 428
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RESULT 3

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US-09-959-845-2
; Sequence 2, Application US/09959845
; GENERAL INFORMATION:
; APPLICANT: Yoshimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-2
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Query Match      67.2%; Score 1819.5; DB 1; Length 549;
Best Local Similarity 68.2%; Pred. No. 0;
Matches 369; Conservative 35; Mismatches 60; Indels 77; Gaps 9;
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QY      1  MARTLRPSLPCPGGKAQJSSALLGAGLLLPPTPPPLLLLLPLLLFSRLCGALAGPI 60
Db      1  MARTPGAPLPCPGGKAQLSSAFPAAGLLLPAPTTPPLLLLLPLLLFSRLCGALAGSI 60
      61  IVEPHVTAWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGEYQGR 120
      61  IVEPHVTAWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDYQGR 120
      121  VLFKNYSLNDATITLHNIGFSDSGKVIKAVTTPPLGNAQSSTTVTLVPTVSLIKGPD 180
      121  VLFKNYSLNDATITLHNIGFSDSGKVIKAVTTPPLGNAQSSTTVTLVPTVSLIKGPD 180
      181  LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISOYKLFPTFRFAR 240
      181  LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISOYKLFPTFRFAR 240
      241  GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
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Db      241  GRRITCVVHKPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPF 300
      301  KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVIYISDVPP 360
      301  KSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQOKVIYISDPPT 360
      361  KOT-----SSIA-----VAGAVIGAVLALFIIA 383
      361  ITTLOFTVQMHSSPADVQDIATEHKKLPPPLSTLATLKDDTIGTIIASVVGALFLVLVS 420
      384  IFVTVLLTPRKKR-----PSYLDKVIDLPPPTHK-----PPPLYEERSPLPQ 425
      421  ILAGVFCYRRRTFRGDIYFAKNYIIPSDMQKESQIDVLHQDELDSPDSVKKENKNPV-- 478
      426  KDLFOPEHL--PLQTFKEREVGNLQHSNGLNSRFDYEDENPVG-----EDG 471
      479  NNLIRKDYLEEBEKTQW--NNVENLTRF-----ERPMDYYEDLKMGMKMFVSDERYNESEDG 532
      472  I 472
      533  L 533
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Search completed: October 7, 2005, 14:08:24
Job time : 0.001 secs